

GGCGGCGGCA	GCCTCGGCTA	CAGCTTCGGC	GGCGAAGGTC	AGCGCCGACG	GCAGCCGGCA	60
CCTGACGGCG	TGACCGACCC	GAGCCGATTT	CTCTTGGATT	TGGCTACACA	CTTATAGATC	120
TTCTGCACTG	TTTACAGGCA	CAGTTGCTGA	TA TGTTTCA	AG	ATG AGT GGG ATG	174
					Met Ser Gly Met	
					1	
GGA GAA AAT ACC TCT GAC CCC TCC AGG GCA GAG ACA AGA AAG CGC AAG						222
Gly Glu Asn Thr Ser Asp 10	Pro Ser Arg Ala Glu Thr Arg Lys Arg Lys					
						20
GAA TGT CCT GAC CAA CTT GGA CCC AGC CCC AAA AGG AAC ACT GAA AAA						270
Glu Cys Pro Asp Gln Leu Gly Pro Ser Pro Lys Arg Asn Thr Glu Lys						
						35
CGT AAT CGT GAA CAG GAA AAT AAA TAT ATA GAA GAA CTT GCA GAG TTG						318
Arg Asn Arg Glu Gln Glu Asn Lys Tyr Ile Glu Glu Leu Ala Glu Leu						
						50
ATT TTT GCA AAT TTT AAT GAT ATA GAC AAC TTT AAC TTC AAA CCT GAC						366
Ile Phe Ala Asn Phe Asn Asp Ile Asp Asn Phe Asn Phe Lys Pro Asp						
						65
AAA TGT GCA ATC TTA AAA GAA ACT GTG AAG CAA ATT CGT CAG ATC AAA						414
Lys Cys Ala Ile Leu Lys Glu Thr Val Lys Gln Ile Arg Gln Ile Lys						
						80
GAA CAA GAG AAA GCA GCA GCT GCC AAC ATA GAT GAA GTG CAG AAG TCA						462
Glu Gln Glu Lys Ala Ala Ala Asn Ile Asp Glu Val Gln Lys Ser						
						95
						100

FIG. 1A

GAT GTA TCC TCT ACA GGG CAG GGT GTC ATC GAC AAG GAT GCG CTG GGG Asp Val Ser Ser 105 Thr Gly Gln Gly Val 110 Ile Asp Lys Asp Ala 115 Leu Gly	510
CCT ATG ATG CTT GAG GCC CTT GAT GGG TTC TTC TTT GTA GTG AAC CTG Pro Met Met Leu 120 Glu Ala Leu Asp 125 Gly Phe Phe Val 130 Val Asn Leu	558
GAA GGC AAC GTT GTG TTT GTG TCA GAG AAT GTG ACA CAG TAT CTA AGG Glu Gly Asn Val 135 Val Phe Val 140 Ser Glu Asn Val 145 Thr Gln Tyr Leu Arg	606
TAT AAC CAA GAA GAG CTG ATG AAC AAA AGT GTA TAT AGC ATC TTG CAT Tyr Asn Gln Glu 150 Glu Leu 155 Met Asn Lys Ser Val 160 Tyr Ser Ile Leu His	654
GTT GGG GAC CAC ACG GAA TTT GTC AAA AAC CTG CTG CCA AAG TCT ATA Val Gly Asp His Thr 165 Glu Phe Val 170 Lys Asn Leu Leu Pro Lys Ser 180 Ile	702
GTA AAT GGG GGA TCT TGG TCT GGC GAA CCT CCG AGG CGG AAC AGC CAT Val Asn Gly Gly 185 Ser Trp Ser Gly Glu 190 Pro Pro Arg Arg Asn Ser His 195	750
ACC TTC AAT TGT CGG ATG CTG GTA AAA CCT TTA CCT GAT TCA GAA GAG Thr Phe Asn Cys 200 Arg Met Leu Val 205 Lys Pro Leu Pro Asp Ser Glu Glu 210	798
GAG GGT CAT GAT AAC CAG GAA GCT CAT CAG AAA TAT GAA ACT ATG CAG Glu Gly His Asp Asn 215 Gln Glu Ala His Gln Lys Tyr 220 Glu Thr Met Gln 225	846

FIG.1B

TGC TTC GCT GTC TCT CAA CCA AAG TCC ATC AAA GAA GAA GGA GAA GAT Cys Phe Ala Val Ser Gln Pro Lys Ser Ile Lys Glu Glu Gly Glu Asp 230 235 240	894
TTG CAG TCC TGC TTG ATT TGC GTG GCA AGA AGA GTT CCC ATG AAG GAA Leu Gln Ser Cys Leu Ile Cys Val Ala Arg Arg Val Pro Met Lys Glu 245 250 255 260	942
AGA CCA GTT CTT CCC TCA TCA GAA AGT TTT ACT ACT CGC CAG GAT CTC Arg Pro Val Leu Pro Ser Ser Glu Ser Phe Thr Thr Arg Gln Asp Leu 265 270 275	990
CAA GGC AAG ATC ACG TCT CTG GAT ACC AGC ACC ATG AGA GCA GCC ATG Gln Gly Lys Ile Thr Ser Ser Leu Asp Thr Ser Thr Met Arg Ala Ala Met 280 285 290	1038
AAA CCA GGC TGG GAG GAC CTG GTA AGA AGG TGT ATT CAG AAG TTC CAT Lys Pro Gly Trp Glu Asp Leu Val Arg Arg Cys Ile Gln Lys Phe His 295 300 305	1086
GCG CAG CAT GAA GGA GAA TCT GTG TCC TAT GCT AAG AGG CAT CAT CAT Ala Gln His Glu Gly Glu Ser Val Ser Tyr Ala Lys Arg His His His 310 315 320	1134
GAA GTA CTG AGA CAA GGA TTG GCA TTC AGT CAA ATC TAT CGT TTT TCC Glu Val Leu Arg Gln Gly Leu Ala Phe Ser Gln Ile Tyr Arg Phe Ser 325 330 335 340	1182
TTG TCT GAT GGC ACT CTT GTT GCT GCA CAA ACG AAG AGC AAA CTC ATC Leu Ser Asp Gly Thr Leu Val Ala Ala Gln Thr Lys Ser Lys Leu Ile 345 350 355	1230

FIG.1C

CGT TCT CAG ACT ACT AAT GAA CCT CAA CTT GTA ATA TCT TTA CAT ATG Arg Ser Gln Thr Thr Asn Glu Pro Gln Leu Val Ile Ser 370	1278
CTT CAC AGA GAG CAG AAT GTG TGT GTG ATG AAT CCG GAT CTG ACT GGA Leu His Arg Glu Gln Asn Val Cys Val Met Asn Pro Asp Leu Thr Gly 385	1326
CAA ACG ATG GGG AAG CCA CTG AAT CCA ATT AGC TCT AAC AGC CCT GCC Gln Thr Met Gly Lys Pro Leu Asn Pro Ile Ser Ser Asn Ser Pro Ala 400	1374
CAT CAG GCC CTG TGC AGT GGT AAC CCA GGT CAG GAC ATG ACC CTC AGT His Gln Ala Leu Cys Ser Gly Asn Pro Gly Gln Asp Met Thr Leu Ser 420	1422
AGC AAT ATA AAT TTT CCC ATA AAT GGC CCA AAG GAA CAA ATG GGC ATG Ser Asn Ile Asn Phe Pro Ile Asn Gly Pro Lys Glu Gln Met Gly Met 435	1470
CCC ATG GGC AGG TTT GGT GGT TCT GGG GGA ATG AAC CAT GTG TCA GGC Pro Met Gly Arg Phe Gly Gly Ser Gly Gly Met Asn His Val Ser Gly 450	1518
ATG CAA GCA ACC ACT CCT CAG GGT AGT AAC TAT GCA CTC AAA ATG AAC Met Gln Ala Thr Thr Pro Gln Gly Ser Asn Tyr Ala Leu Lys Met Asn 465	1566
AGC CCC TCA CAA AGC AGC CCT GGC ATG AAT CCA GGA CAG CCC ACC TCC Ser Pro Ser Gln Ser Ser Pro Pro Gly Met Asn Pro Gly Gln Pro Thr Ser 480	1614

FIG.1D

ATG CTT TCA CCA AGG CAT CGC ATG AGC CCT GGA GTG GCT GGC AGC CCT 1662  
Met Leu Ser Pro Arg Arg His Arg Met Ser Pro Gly Val Ala Gly Ser Pro  
485 490 495 500

CGA ATC CCA CCC AGT AGT CAG TTT TCC CCT GCA GGA AGC TTG CAT TCC CCT 1710  
Arg Ile Pro Pro Ser Ser Phe Ser Pro Ala Gly Ser Leu His Ser Pro  
505 510 515

GTG GGA GTT TGC AGC AGC ACA GGA AAT AGC CAT AGT TAT ACC AAC AGC 1758  
Val Gly Val Cys Ser Ser Thr Gly Asn Ser His Ser Tyr Thr Asn Ser  
520 530 535

TCC CTC AAT GCA CTT CAG GCC CTC AGC GAG GGC CAC GGG GTC TCA TTA 1806  
Ser Leu Asn Ala Leu Gln Ala Leu Ser Glu Gly His Gly Val Ser Leu  
535 540 545

GGG TCA TCG TTG GCT TCA CCA GAC CTA AAA ATG GGC AAT TTG CAA AAC 1854  
Gly Ser Ser Leu Ala Ser Pro Asp Leu Lys Met Gly Asn Leu Gln Asn  
550 555 560

TCC CCA GTT AAT ATG AAT CCT CCC CCA CTC AGC AAG ATG GGA AGC TTG 1902  
Ser Pro Val Asn Met Asn Pro Pro Pro Leu Ser Lys Met Gly Ser Leu  
565 570 575 580

GAC TCA AAA GAC TGT TTT GGA CTA TAT GGG GAG CCC TCT GAA GGT ACA 1950  
Asp Ser Lys Asp Cys Phe Gly Leu Tyr Gly Glu Pro Ser Glu Gly Thr  
585 590 595

ACT GGA CAA GCA GAG AGC AGC TGC CAT CCT GGA GAG CAA AAG GAA ACA 1998  
Thr Gly Gln Ala Glu Ser Ser Cys His Pro Gly Glu Lys Glu Thr  
600 605 610

FIG.1E

AAT GAC CCC AAC CTG CCC CCG GCC GTG AGC AGT GAG AGA GCT GAC GGG Asn Asp Pro Asn Leu Pro Pro Ala Val Ser Ser Glu Arg Ala Asp Gly 615 620 625	2046
CAG AGC AGA CTG CAT GAC AGC AAA GGG CAG ACC AAA CTC CTG CAG CTG Gln Ser Arg Leu His Asp Ser Lys Gly Gln Thr Lys Leu Leu Gln Leu 630 635 640	2094
CTG ACC ACC AAA TCT GAT CAG ATG GAG CCC TCG CCC TTA GCC AGC TCT Leu Thr Thr Lys Ser Asp Gln Met Glu Pro Ser Pro Leu Ala Ser 645 650 655 660	2142
TTG TCG GAT ACA AAC AAA GAC TCC ACA GGT AGC TTG CCT GGT TCT GGG Leu Ser Asp Thr Asn Lys Asp Ser Thr Gly Ser Leu Pro Gly Ser Gly 665 670 675	2190
TCT ACA CAT GGA ACC TCG CTC AAG GAG AAG CAT AAA ATT TTG CAC AGA Ser Thr His Gly Thr Ser Leu Lys Glu Lys His Lys Ile Leu His Arg 680 685 690	2238
CTC TTG CAG GAC AGC AGT TCC CCT GTG GAC TTG GCC AAG TTA ACA GCA Leu Leu Gln Asp Ser Ser Ser Pro Val Asp Leu Ala Lys Leu Thr Ala 695 700 705	2286
GAA GCC ACA GGC AAA GAC CTG AGC CAG GAG TCC AGC AGC ACA GCT CCT Glu Ala Thr Gly Lys Asp Leu Ser Ser Gln Glu Ser Ser Thr Ala Pro 710 715 720	2334
GGA TCA GAA GTG ACT ATT AAA CAA GAG CCG GTG AGC CCC AAG AAG AAA Gly Ser Glu Val Thr Ile Lys Lys Gln Glu Pro Val Ser Pro Lys Lys 725 730 735 740	2382

FIG. 1F

# T09240" 9224360

GAG AAT GCA CTA CTT CGC TAT TTG CTA GAT AAA GAT ACT AAA GAT Glu Asn Ala Leu Leu Arg Tyr Leu Leu Asp Lys Asp Thr Lys Asp 745 750 755	2430
ATT GGT TTA CCA GAA ATA ACC CCC AAA CTT GAG AGA CTG GAC AGT AAG Ile Gly Leu Pro Glu Ile Thr Pro Lys Leu Glu Arg Leu Asp Ser Lys 760 765 770	2478
ACA GAT CCT GCC AGT AAC ACA AAA TTA ATA GCA ATG AAA ACT GAG AAG Thr Asp Pro Ala Ser Asn Thr Lys Leu Ile Ala Met Lys Thr Glu Lys 775 780 785	2526
GAG GAG ATG AGC TTT GAG CCT GGT GAC CAG CCT GGC AGT GAG CTG GAC Glu Glu Met Ser Phe Glu Pro Gly Asp Gln Pro Gly Ser Glu Leu Asp 790 795 800	2574
AAC TTG GAG GAG ATT TTG GAT GAT TTG CAG AAT AGT CAA TTA CCA CAG Asn Leu Glu Glu Ile Leu Asp Asp Leu Gln Asn Ser Gln Leu Pro Gln 805 810 815 820	2622
CTT TTC CCA GAC ACG AGG CCA GGC GCC CCT GCT GGA TCA GTT GAC AAG Leu Phe Pro Asp Thr Arg Pro Gly Ala Pro Ala Gly Ser Val Asp Lys 825 830 835	2670
CAA GCC ATC ATC AAT GAC CTC CTG CAA CTC ACA GCT GAA AAC AGC CCT Gln Ala Ile Ile Asn Asp Leu Met Gln Leu Thr Ala Glu Asn Ser Pro 840 845 850	2718
GTC ACA CCT GTT GGA GCC CAG AAA ACA GCA CTG CGA ATT TCA CAG AGC Val Thr Pro Val Gly Ala Gln Lys Thr Ala Leu Arg Ile Ser Gln Ser 855 860 865	2766

FIG.1G

ACT TTT AAT AAC CCA CGA CCA GGG CAA CTG GGC AGG TTA TTG CCA AAC Thr Phe Asn Asn Pro Arg 875 870	2814
CAG AAT TTA CCA CTT GAC ATC ACA TTG CAA AGC CCA ACT GGT GCT GGA Gln Asn Leu Pro Leu 890 885	2862
CCT TTC CCA CCA ATC AGA AAC AGT AGT CCC TAC TCA GTG ATA CCT CAG Pro Phe Pro Pro Ile Arg Asn Ser 910 905	2910
CCA GGA ATG ATG GGT AAT CAA GGG ATG ATA GGA AAC CAA GGA AAT TTA Pro Gly Met Met Gly Asn Gln Gly Met Ile Gly Asn Gln 930 920	2958
GGG AAC AGT AGC ACA GGA ATG ATT GGT AAC AGT GCT TCT CGG CCT ACT Gly Asn Ser Ser Thr Gly Met Ile Gly Asn Ser Ala Ser Arg Pro Thr 945 935	3006
ATG CCA TCT GGA GAA TGG GCA CCG CAG AGT TCG GCT GTG AGA GTC ACC Met Pro Ser Gly Glu Trp Ala Pro Gln Ser Ser Ala Val Arg Val Thr 960 950	3054
TGT GCT GCT ACC ACC AGT GCC ATG AAC CGG CCA GTC CAA GGA GGT ATG Cys Ala Ala Thr Thr Ser Ala Met Asn Arg Pro Val Gln Gly Gly Met 975 965	3102
ATT CGG AAC CCA GCA GCC AGC ATC CCC ATG AGG CCC AGC AGC CAG CCT Ile Arg Asn Pro Ala Ala Ser Ile Pro Met Arg Pro Ser Ser Gln Pro 990 985	3150

FIG.1H



GGC CAA AGA CAG ACG CTT CAG TCT CAG GTC ATG AAT ATA GGG CCA TCT  
Gly Gln Arg Gln Thr 1000  
1005  
1010 3198

GAA TTA GAG ATG AAC ATG GGG GGA CCT CAG TAT AGC CAA CAA CAA GCT  
Glu Leu Glu Met Asn Met Gly Gly Pro Gln Tyr Ser Gln Gln Gln Ala  
1015  
1020 3246

CCT CCA AAT CAG ACT GCC CCA TGG CCT GAA AGC ATC CTG CCT ATA GAC  
Pro Pro Asn Gln Thr Ala Pro Trp Pro Glu Ser Ile Leu Pro Ile Asp  
1030  
1035 3294

CAG GCG TCT TTT GCC AGC CAA AAC AGG CAG CCA TTT GGC AGT TCT CCA  
Gln Ala Ser Phe Ala 1045  
1050 3342

GAT GAC TTG CTA TGT CCA CAT CCT GCA GCT GAG TCT CCG AGT GAT GAG  
Asp Asp Leu Leu Cys Pro His Pro Ala Ala Glu Ser Pro Ser Asp Glu  
1065  
1070 3390

GGA GCT CTC CTG GAC CAG CTG TAT CTG GCC TTG CGG AAT TTT GAT GGC  
Gly Ala Leu Leu Asp Gln Leu Tyr Leu Ala Leu Arg Asn Phe Asp Gly  
1080  
1085 3438

CTG GAG GAG ATT GAT AGA GCC TTA GGA ATA CCC GAA CTG GTC AGC CAG  
Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Ser Gln  
1095  
1100 3486

AGC CAA GCA GTA GAT CCA GAA CAG TTC TCA AGT CAG GAT TCC AAC ATC  
Ser Gln Ala Val Asp Pro Glu Gln Phe Ser Ser Gln Asp Ser Asn Ile  
1110  
1115 3534

FIG.11

ATG CTG GAG CAG AAG GCG CCC GTT TTC CCA CAG CAG TAT GCA TCT CAG Met Leu Glu Gln Lys Ala Pro Val Phe Pro Gln Gln Tyr Ala Ser Gln 1125 1130 1135 1140	3582
GCA CAA ATG GCC CAG GGT AGC TAT TCT CCC ATG CAA GAT CCA AAC TTT Ala Gln Met Ala Gln Gly Ser Tyr Ser Pro Met Gln Asp Pro Asn Phe 1145 1150 1155	3630
CAC ACC ATG GGA CAG CGG CCT AGT TAT GCC ACA CTC CGT ATG CAG CCC His Thr Met Gly Gln Arg Pro Ser Tyr Ala Thr Leu Arg Met Gln Pro 1160 1165 1170	3678
AGA CCG GGC CTC AGG CCC ACG GGC CTA GTG CAG AAC CAG CCA AAT CAA Arg Pro Gly Leu Arg Pro Thr Gly Leu Val Gln Asn Gln Pro Asn Gln 1175 1180 1185	3726
CTA AGA CTT CAA CTT CAG CAT CGC CTC CAA GCA CAG CAG AAT CGC CAG Leu Arg Leu Gln Leu Gln His Arg Leu Gln Ala Gln Gln Asn Arg Gln 1190 1195 1200	3774
CCA CTT ATG AAT CAA ATC AGC AAT GTT TCC AAT GTG AAC TTG ACT CTG Pro Leu Met Asn Gln Ile Ser Asn Val Ser Asn Val Asn Leu Thr Leu 1205 1210 1215 1220	3822
AGG CCT GGA GTA CCA ACA CAG GCA CCT ATT AAT GCA CAG ATG CTG GCC Arg Pro Gly Val Pro Thr Gln Ala Pro Ile Asn Ala Gln Met Leu Ala 1225 1230 1235	3870
CAG AGA CAG AGG GAA ATC CTG AAC CAG CAT CTT CGA CAG AGA CAA ATG Gln Arg Gln Arg Glu Ile Leu Asn Gln His Leu Arg Gln Arg Gln Met 1240 1245 1250	3918

FIG.1J

CAT CAG CAA CAG CAA GTT CAG CAA CGA ACT TTG ATG ATG AGA GGA CAA His Gln Gln Gln Val Gln 1260 1255	3966
GGG TTG AAT ATG ACA CCA AGC ATG GTG GCT CCT AGT GGT ATG CCA GCA Gly Leu Asn Met Thr Pro Ser Met Val Ala Pro Ser Gly Met Pro Ala 1270 1275	4014
ACT ATG AGC AAC CCT CGG ATT CCC CAG GCA AAT GCA CAG CAG TTT CCA Thr Met Ser Asn Pro Arg Ile Pro Gln Ala Asn Ala Gln Gln Phe 1285 1290	4062
TTT CCT CCA AAC TAC GGA ATA AGT CAG CAA CCT GAT CCA GGC TTT ACT Phe Pro Pro Asn Tyr Gly Ile Ser Gln Gln Pro Asp Pro Gly Phe Thr 1305 1310	4110
GGG GCT ACG ACT CCC CAG AGC CCA CTT ATG TCA CCC CGA ATG GCA CAT Gly Ala Thr Thr Pro Gln Ser Pro Leu Met Ser Pro Arg Met Ala His 1320 1325	4158
ACA CAG AGT CCC ATG ATG CAA CAG TCT CAG GCC AAC CCA GCC TAT CAG Thr Gln Ser Pro Met Met Gln Gln Ser Gln Ala Asn Pro Ala Tyr Gln 1335 1340	4206
GCC CCC TCC GAC ATA AAT GGA TGG GCG CAG GGG AAC ATG GGC GGA AAC Ala Pro Ser Asp Ile Asn Gly Trp Ala Gln Gly Asn Met Gly Gly Asn 1350 1355	4254
AGC ATG TTT TCC CAG CAG TCC CCA CCA CAC TTT GGG CAG CAA GCA AAC Ser Met Phe Ser Gln Gln Ser Pro Pro His Phe Gly Gln Gln Ala Asn 1365 1370	4302

FIG.1K

ACC AGC ATG TAC AGT AAC AAC ATG AAC ATC AAT GTG TCC ATG GCG ACC 4350  
 Thr Ser Met Tyr 1385 Ser Asn Asn Met Asn Ile Asn Val Ser Met Ala Thr 1395

AAC ACA GGT GGC ATG AGC AGC ATG AAC CAG ATG ACA GGA CAG ATC AGC 4398  
 Asn Thr Gly Gly Met Ser Ser Met Asn Gln Met Thr Gly Gln Ile Ser 1400 1405 1410

ATG ACC TCA GTG ACC TCC GTG TCT ACG TCA GGG CTG TCC TCC ATG GGT 4446  
 Met Thr Ser Val Thr Ser Val Ser Thr Ser Gly Leu Ser Ser Met Gly 1415 1420 1425

CCC GAG CAG GTT AAT GAT CCT GCT CTG AGG GGA GGC AAC CTG TTC CCA 4494  
 Pro Glu Gln Val Asn Asp Pro Ala Leu Arg Gly Gly Asn Leu Phe Pro 1430 1435 1440

AAC CAG CTG CCT GGA ATG GAT ATG ATT AAG CAG GAG GGA GAC ACA ACA 4542  
 Asn Gln Leu Pro Gly Met Asp Met Ile Lys Gln Glu Gly Asp Thr 1445 1450 1455 1460

CGG AAA TAT TGC TGACACTGCT GAAGCCAGTT GCTTCTTCAG CTGACCGGGC 4594  
 Arg Lys Tyr Cys

TCACTTGCTC AAAACACTTC CAGTCTGGAG AGCTGTGTCT ATTTGTTTCA ACCCAACTGA 4654

CCTGCCAGCC GGTTCCTGCTA GAGCAGACAG GCCTGGCCCT GGTTCCTCAGG GTGGCGTCCA 4714

CTCGGCTGTG GCAGGAGGAG CTGCCTCTTC TCTTGACAGT CTGAAGCTCG CATCCAGACA 4774

GTGGCTCAGT CTGTTCCCTG CATTACCTT AGTGCAACTT AGATCTCTCC TCCCCAAGTA 4834

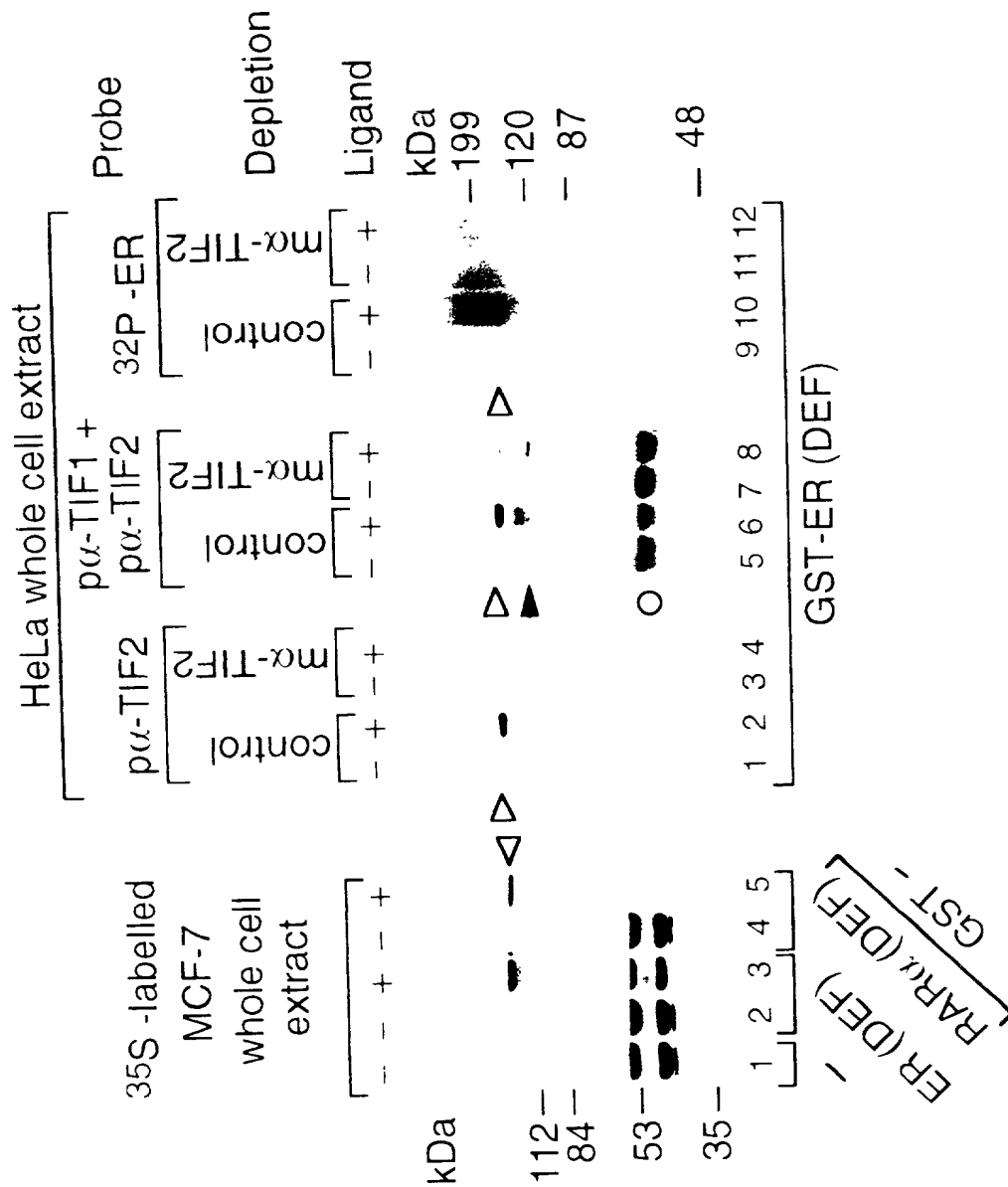
FIG.1L

AATGTTGACA	GGCCAATTC	ATACCCATGT	CAGATTGAAT	GTATTTAAAT	GTATGTATTT	4894
AAGGAGAACC	ATGCTCTTGT	TCTGTTCCTG	TTCGGTTCCA	GACACTGGTT	TCTTGCTTTG	4954
TTTTCCCTGG	CTAACAGTCT	AGTGCCAAAG	ATTAAAGATT	TAICTGGGGG	AAAGAAAAGA	5014
ATTTTTTAAA	AAATTAAACT	AAAGATGTTT	TAAGCTAAAG	CCTGAATTTG	GGATGGAAGC	5074
AGGACAGACA	CCGTGGACAG	CGCTGTATTT	ACAGACACAC	CCAGTCCGTG	AAGACCAACA	5134
AAGTCACAGT	CGTATCTCTA	GAAAGCTCTA	AAGACCATGT	TGGAAAGAGT	CTCCAGTTAC	5194
TGAACAGATG	AAAAGGAGCC	TGTGAGAGGG	CTGTTAACAT	TAGCAAATAT	TTTTTCCTTG	5254
TTTTTCTTT	GTTAAAACCA	AAC TG GTTCA	CCTGAATCAT	GAATTGAGAA	GAATAATTTT	5314
TCATTTCTAA	ATTAAGTCCC	TTTTAGTTTG	ATCAGACAGC	TTGAATCAGC	ATCTCTTCTT	5374
CCCTGTCAGC	CTGACTCTTC	CCCTCCCCCTC	TCATATCCC	CATACTCCCT	ATTTTCATTC	5434
CTTTTTTTAA	AAATAATATA	AGCTACAGAA	ACCAGGTAAG	CCCTTTATTT	CCTTAAATGT	5494
TTTGCCAGCC	ACTTACCAAT	TGCTAAGTAT	TGAATTTTCAG	AAAAAAAAAAA	TGCATTTTACT	5554
GGCAAGGAGA	AGAGCAAAGT	TAAGGCTTGA	TACCAATCGA	GCTAAGGATA	CCTGCTTTGG	5614
AAGCATGTTT	ATTCTGTTCC	CCAGCAACTC	TGGCCTCCAA	AATGGGAGAA	ACGCCAGTGT	5674
GTTTAAATTG	ATAGCAGATA	TCACGACAGA	TTTAACCTCT	GCCATGTGTT	TTTTATTTTG	5734
TTTTTTAGCA	GTGCTGACTA	AGCCGAAGTT	TTGTAAGGTA	CATAAAATCC	AATTTATATG	5794

FIG. 1M

TAAACAAGCA ATAAATTTAAG TTGAGAACTT ATGTGTTTTA ATTGTATAAT TTTTGTGAGG 5854  
 TATACATATT GTGGAATTGA CTCAAAAATG AGGTACTTCA GTATTAAATT AGATACTCTC 5914  
 ATAGCAATGT CTCCTAAAGG TGTTTTGIAA AGGATATCAA TGCCCTTGATT AGACCTAATT 5974  
 TGTAGACTTA AGACTTTTTTA TTTTCTAAAC CTTGTGATTC TGCTTATAAG TCATTTATCT 6034  
 AATCTATATG ATATGCAGCC GCTGTAGGAA CCAATTCTTG ATTTTATAT GTTTATATTC 6094  
 TTTCTTAATG AACCTTAGAA AGACTACATG TTAATAAGCA GGCCACTTTT ATGGTTGTTT 6154  
 TT 6156

FIG.1N



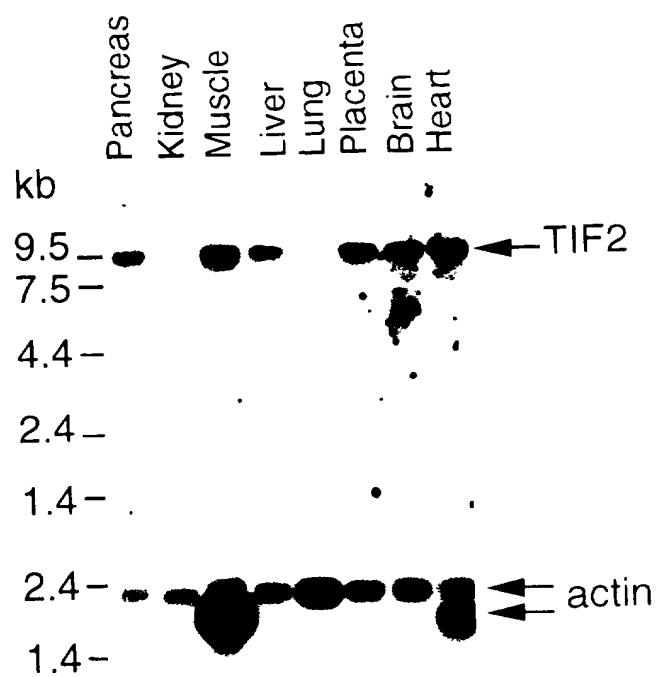


FIG.2C



[illegible]

FIG. 3A



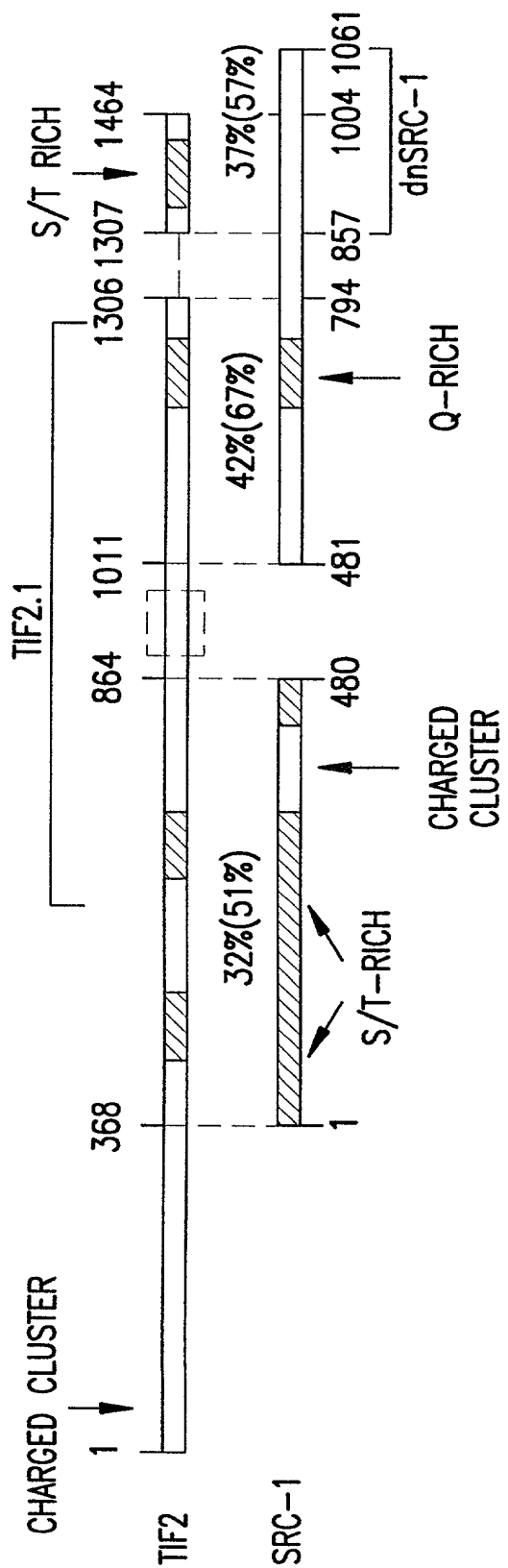
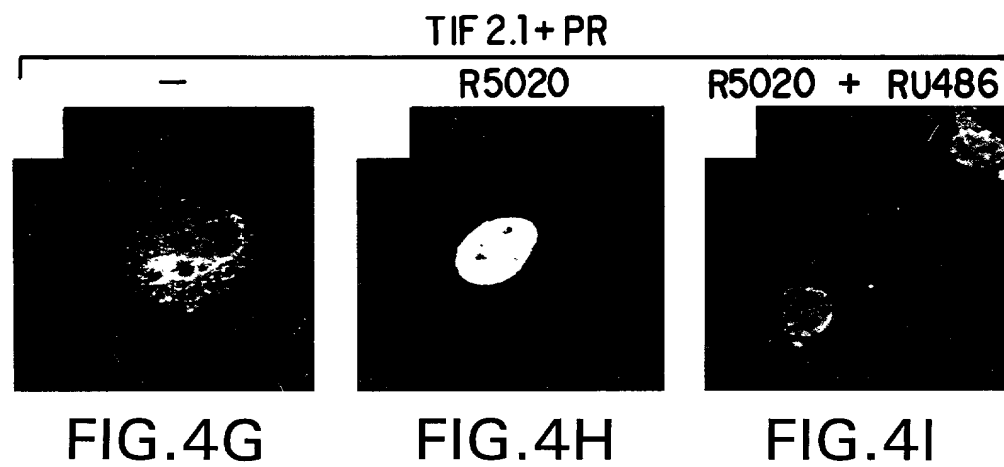
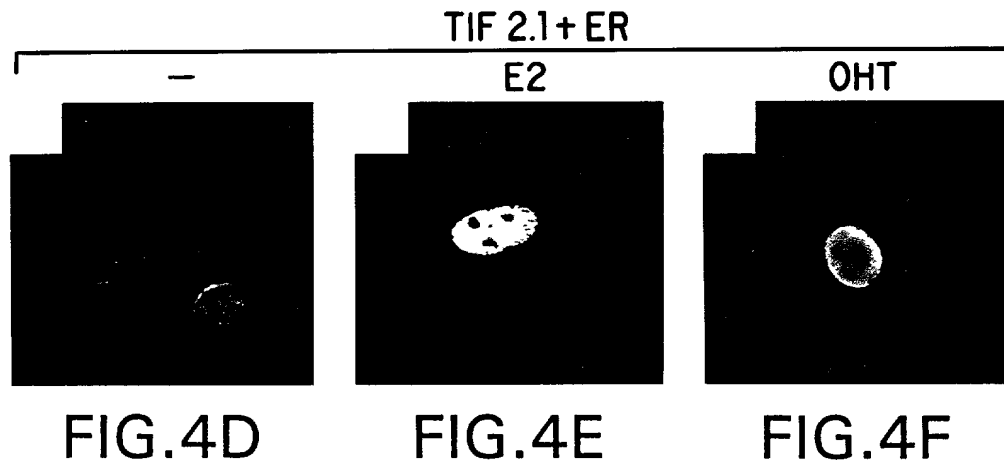
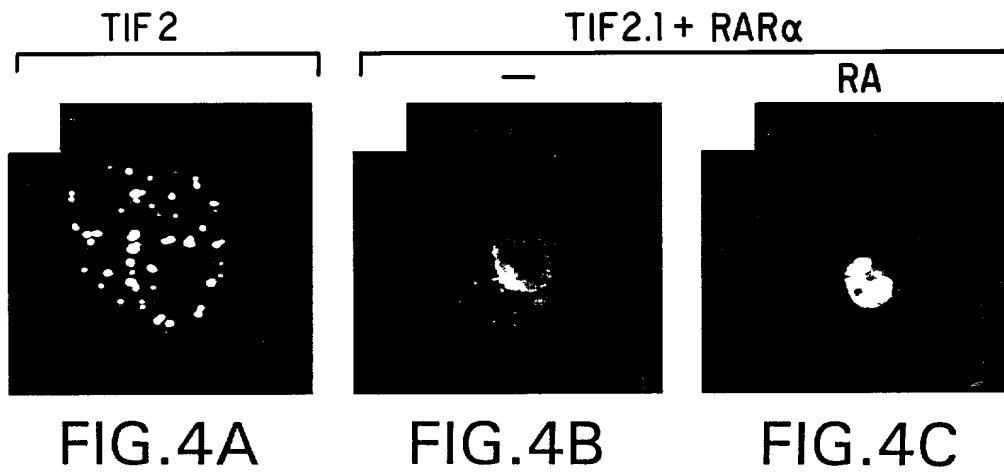


FIG. 3C



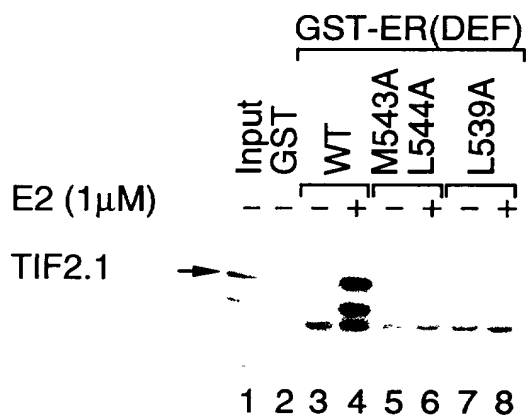


FIG.4K

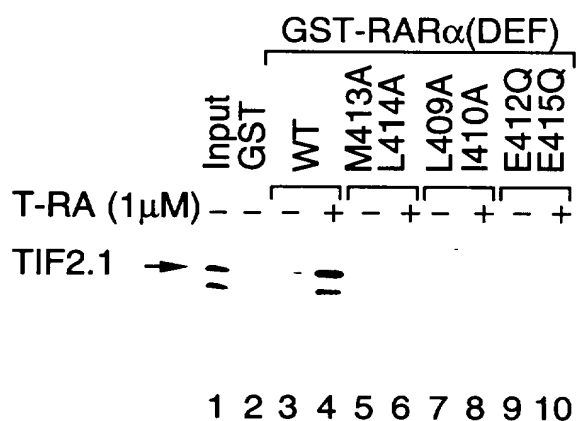


FIG.4L

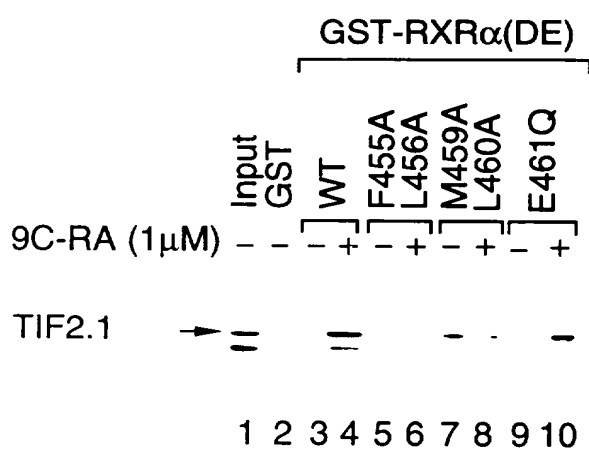


FIG.4M

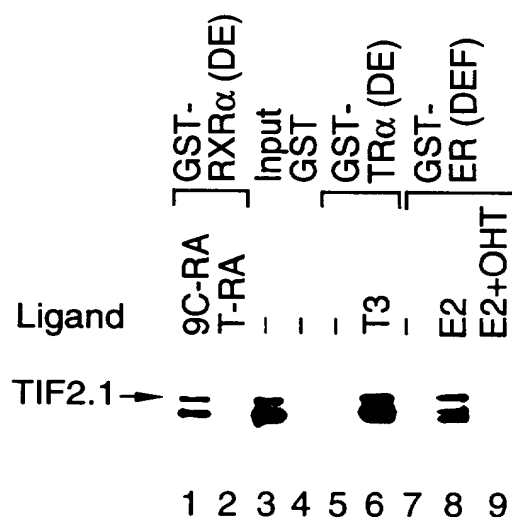


FIG.4N

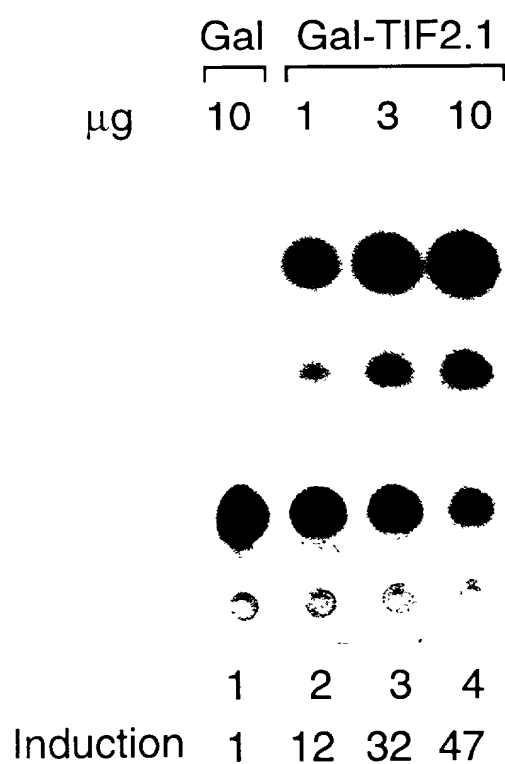


FIG.5A

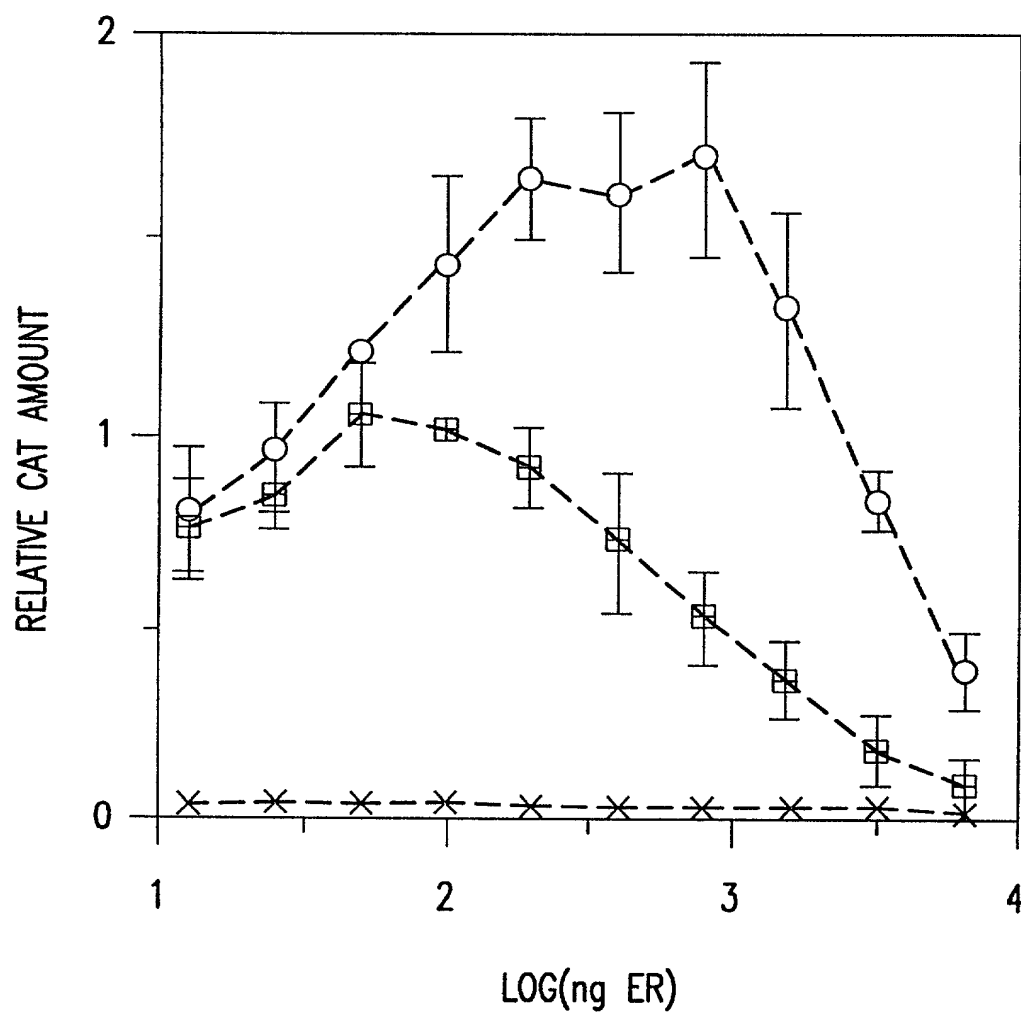


FIG.5B

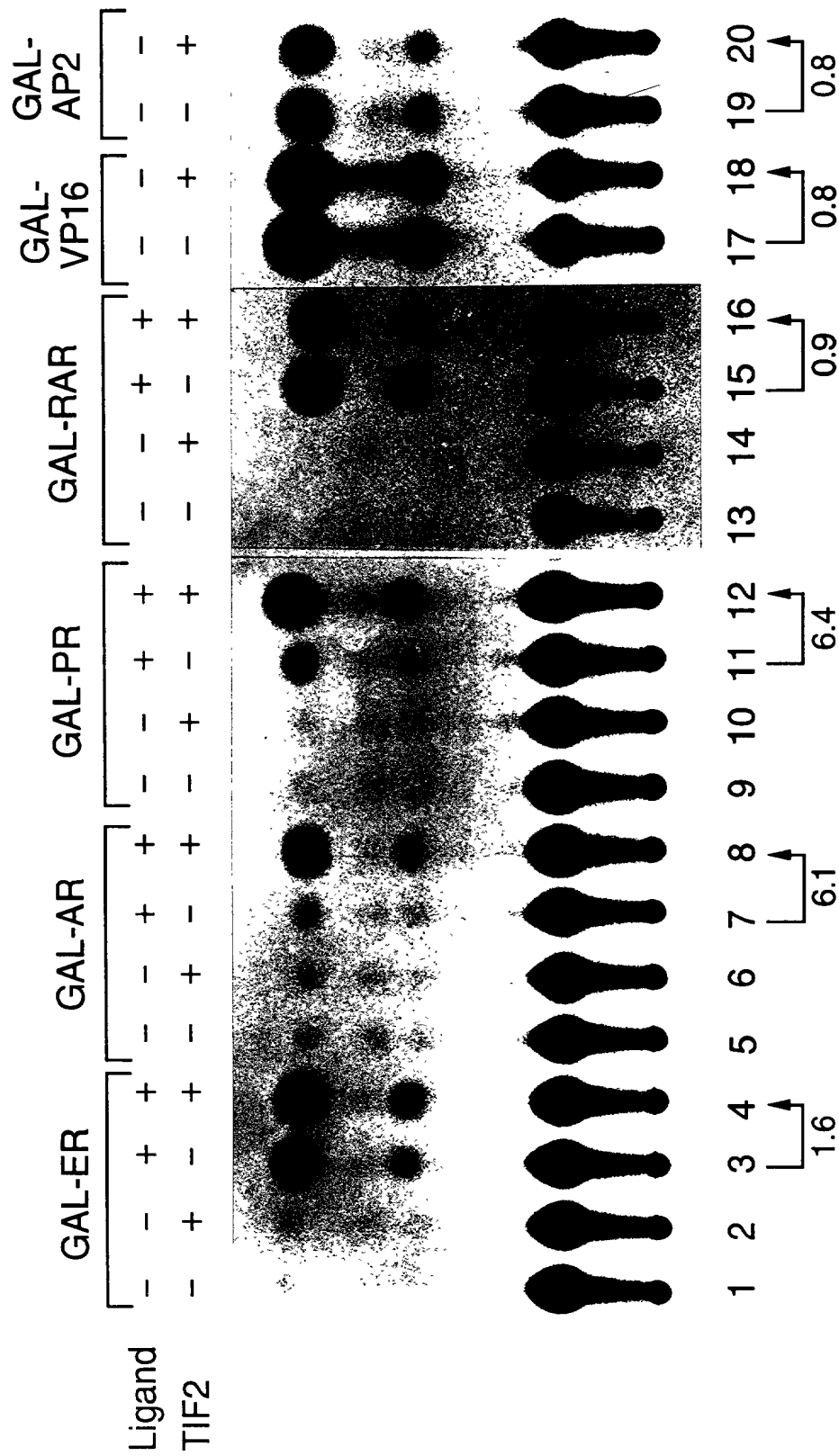


FIG.5C



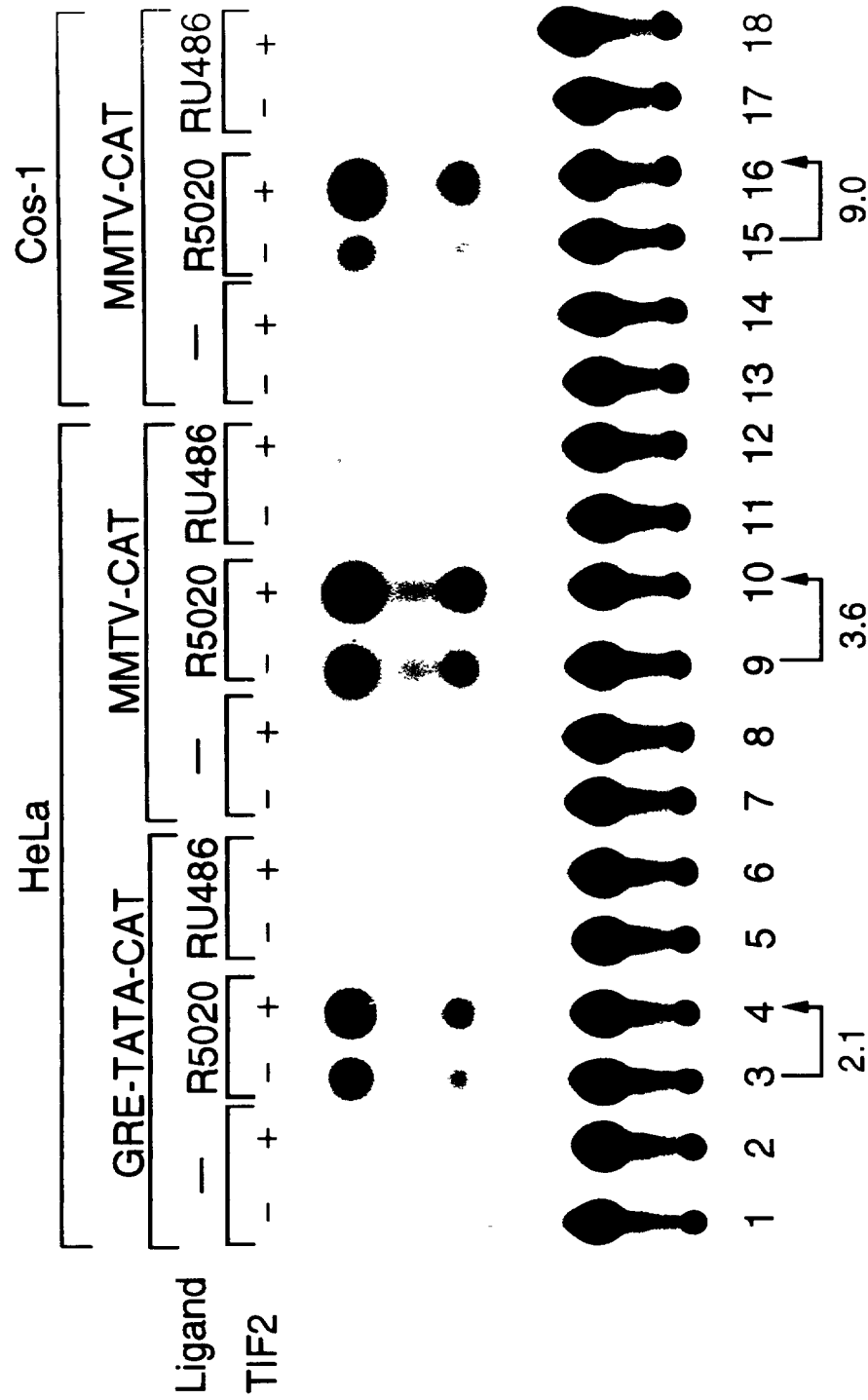
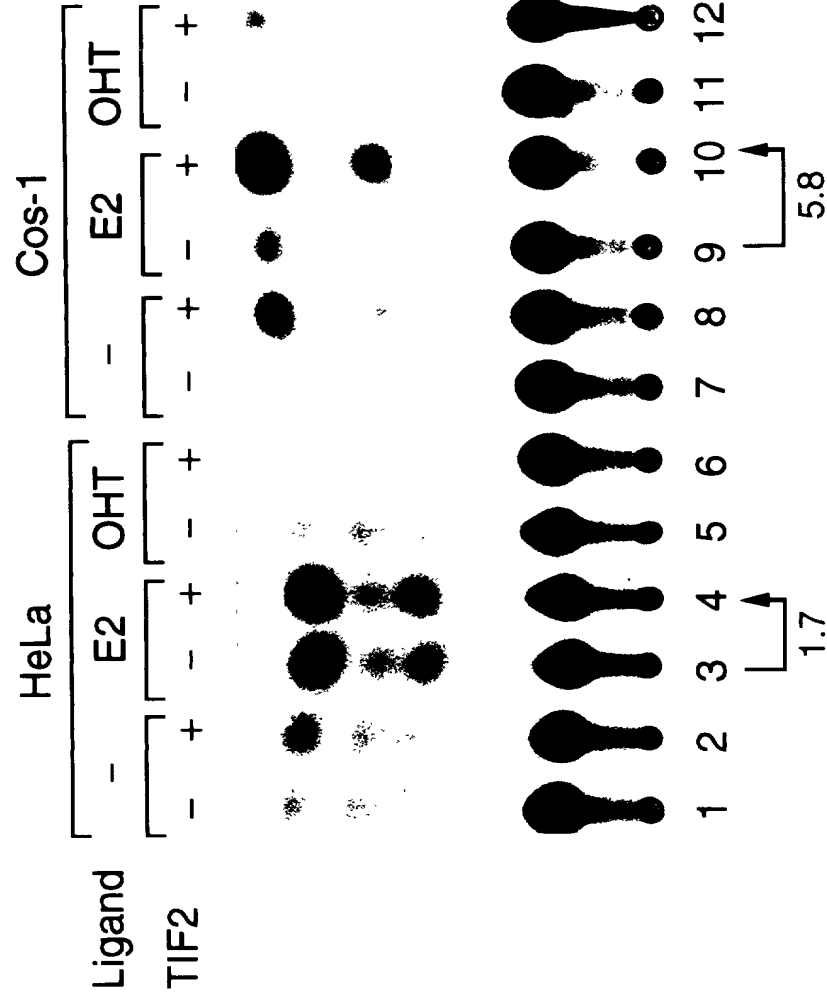


FIG.5D



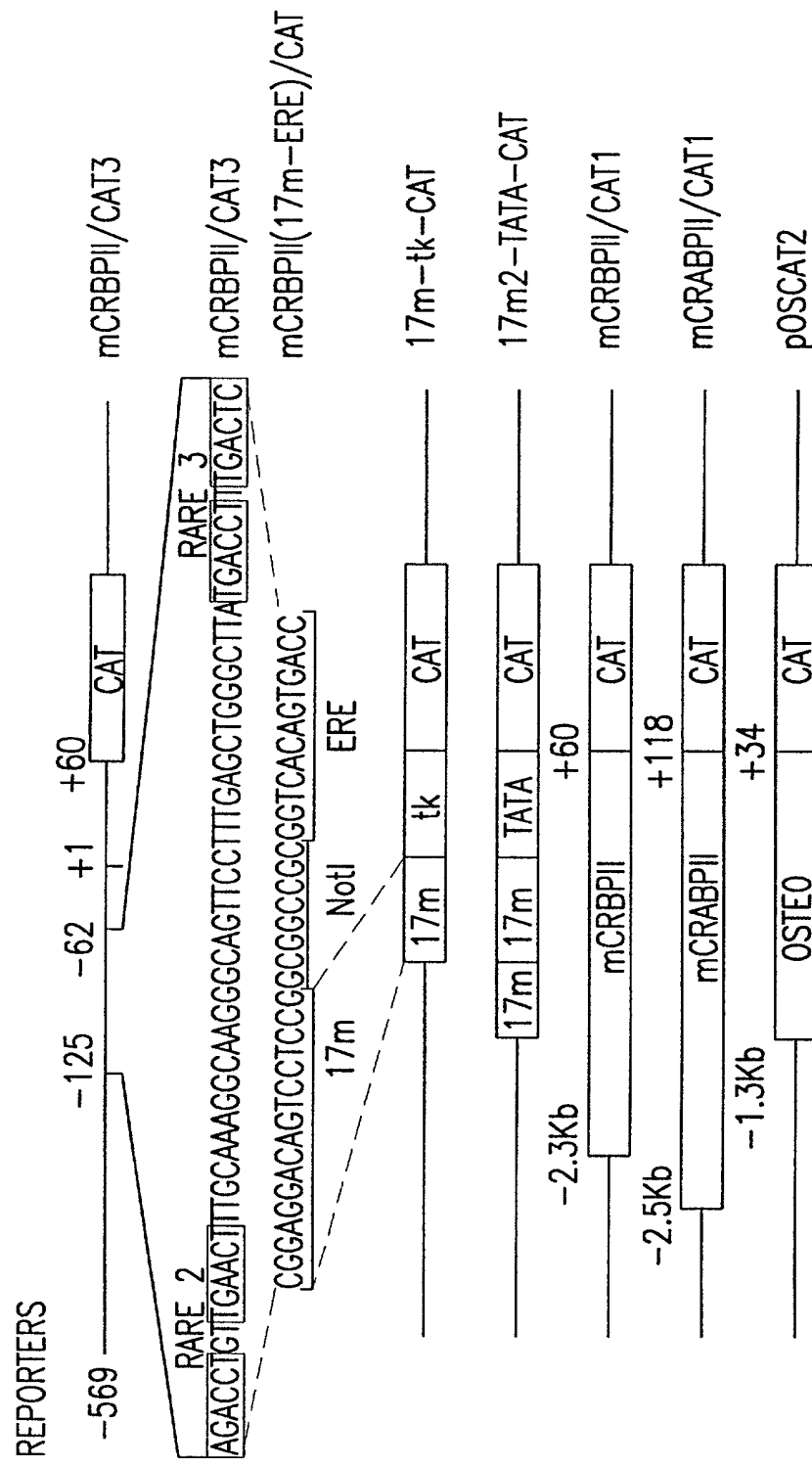


FIG.6A

# RECEPTORS

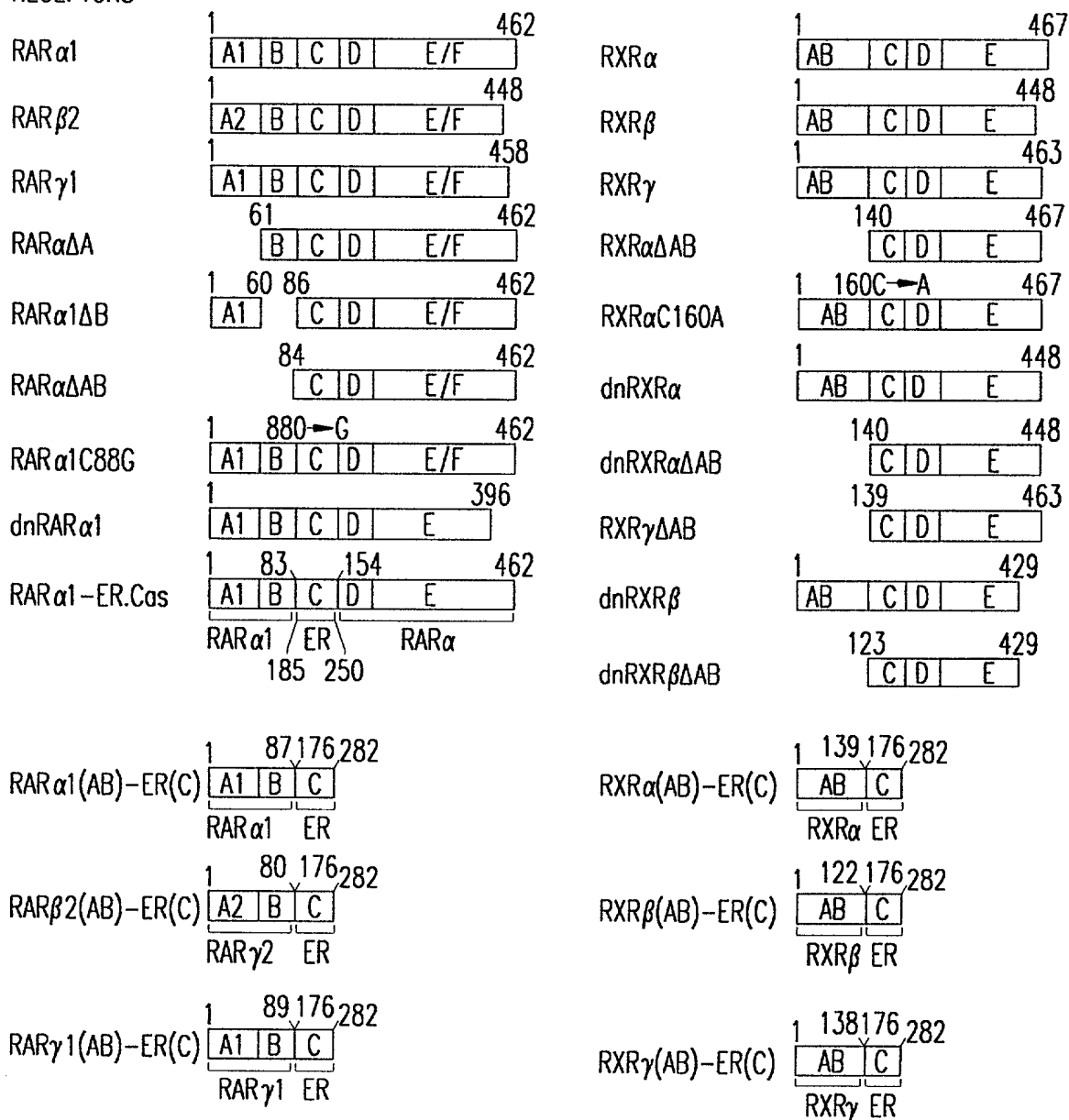


FIG.6B

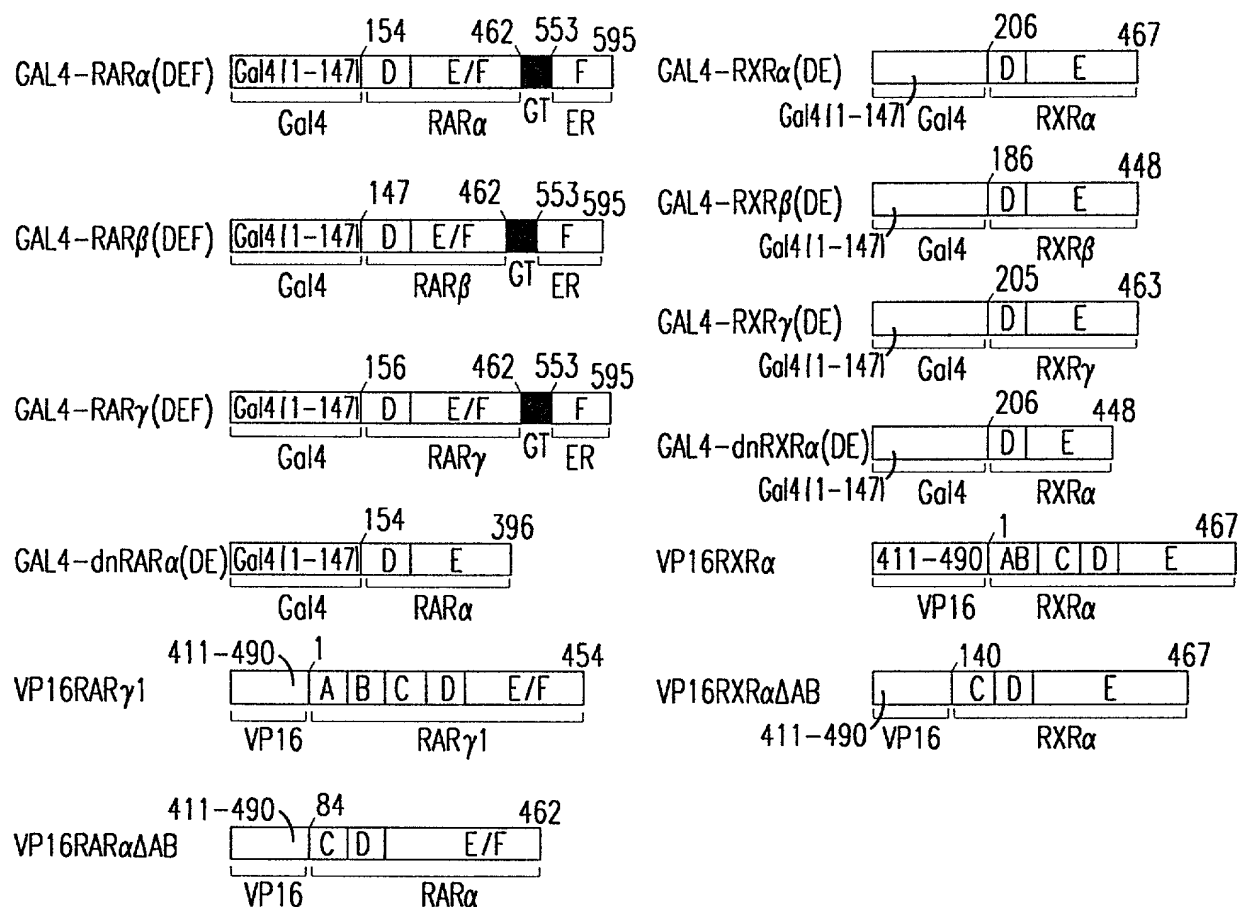


FIG.6C

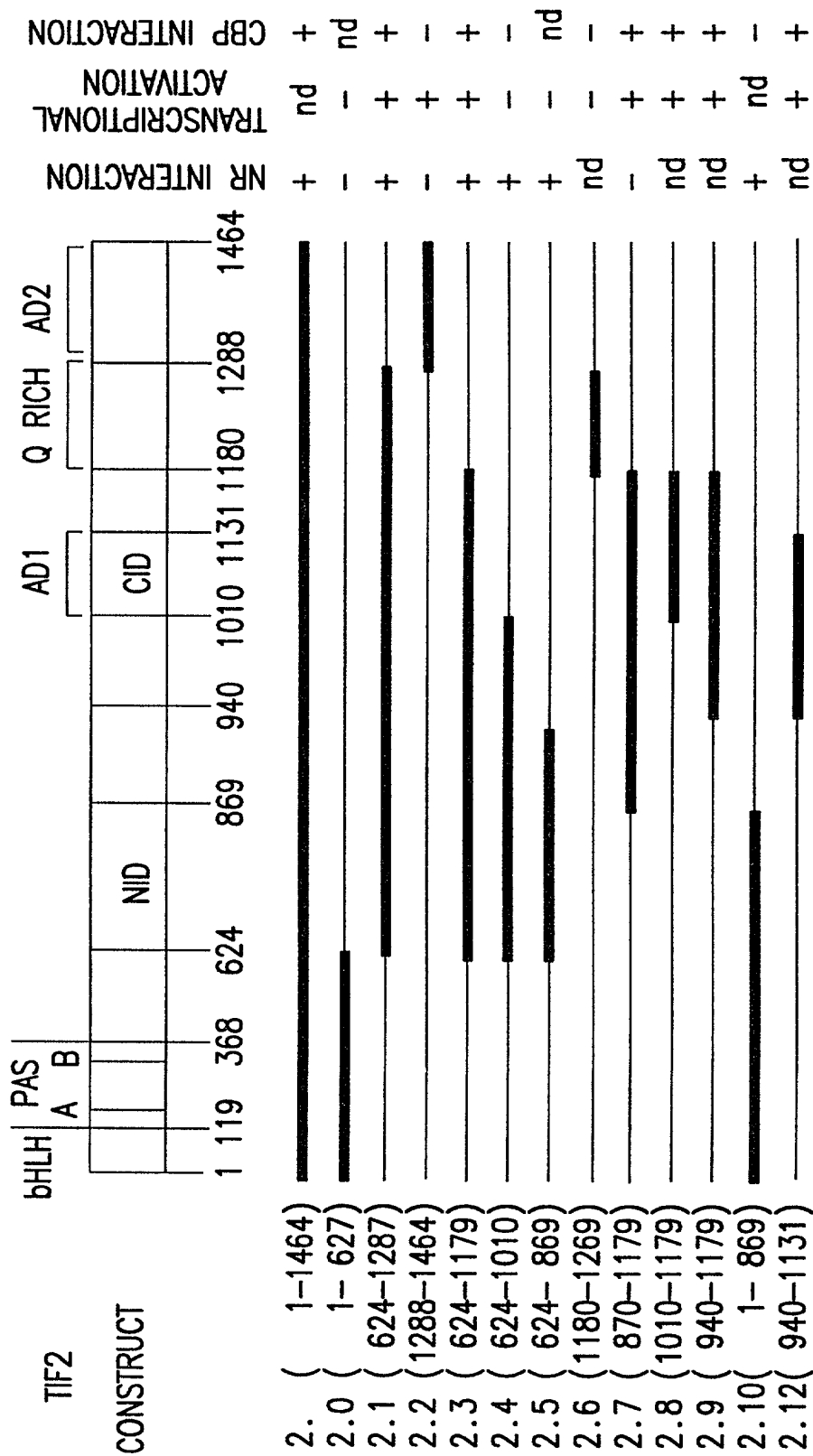


FIG. 7A

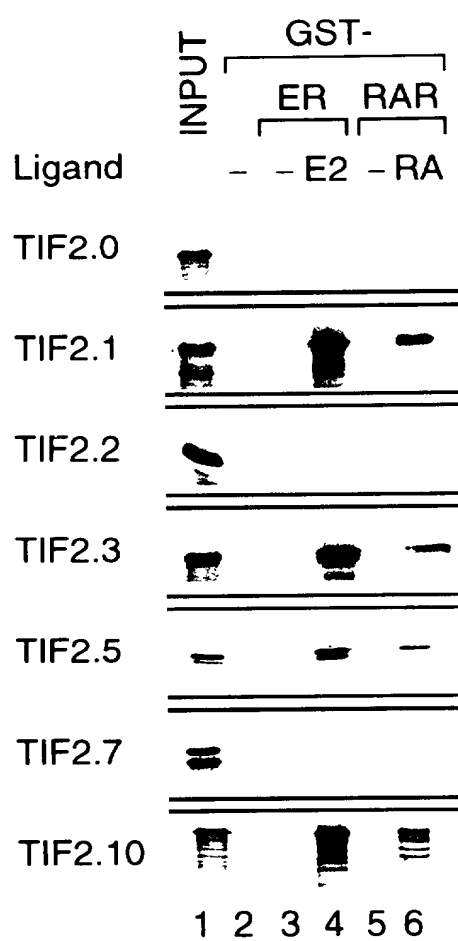


FIG.7B



FIG.7D

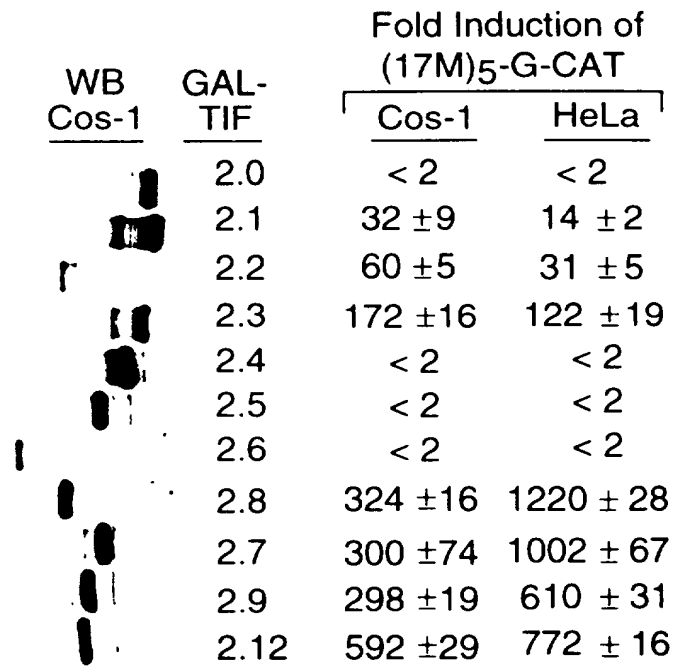


FIG.7C



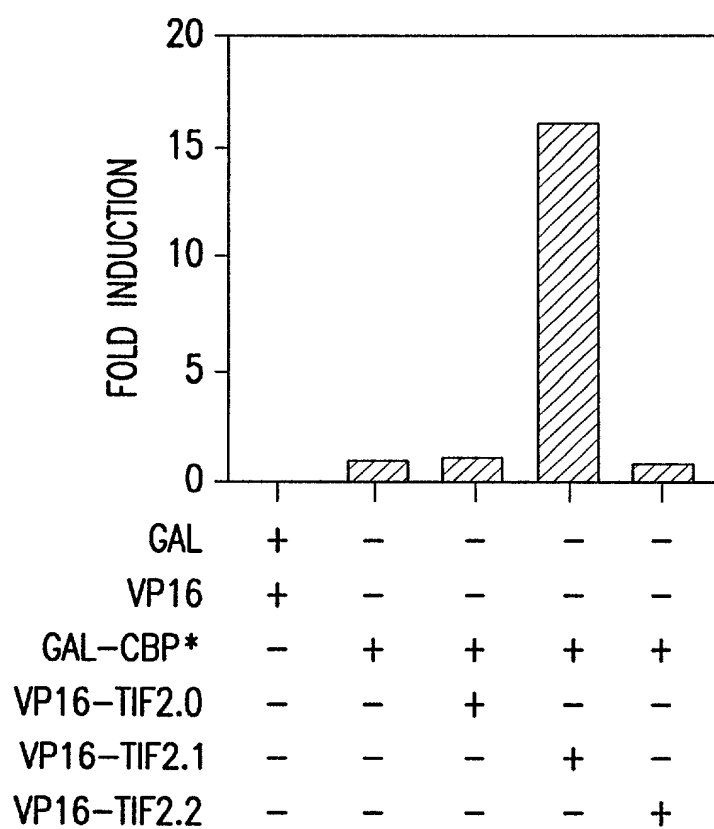


FIG.7E



NR box

TIF1 $\alpha$	724	-	RSILTSLLL	NSS	-	735
RIP140	933	-	FNVLKQLL	SEN	-	944
TRIP3	95	-	SATLRSLLL	NPH	-	106
TIF2(I)	638	-	QTKLLQLL	TTKS	-	648
TIF2(II)	687	-	HKILHRLL	QDSS	-	698
TIF2(III)	742	-	NALLRYLL	DKDD	-	753

FIG.8B

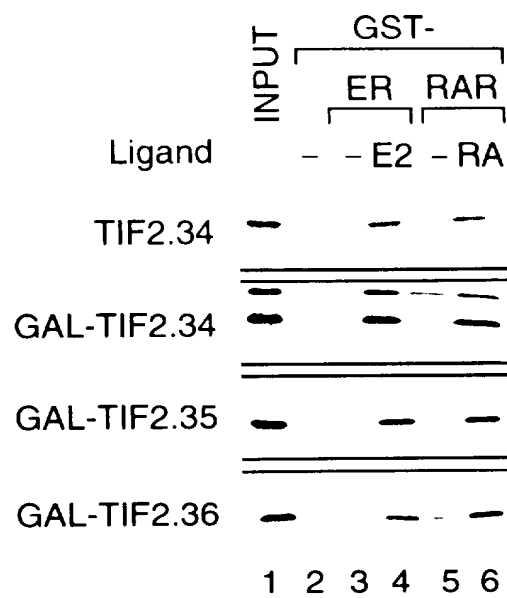


FIG.8C

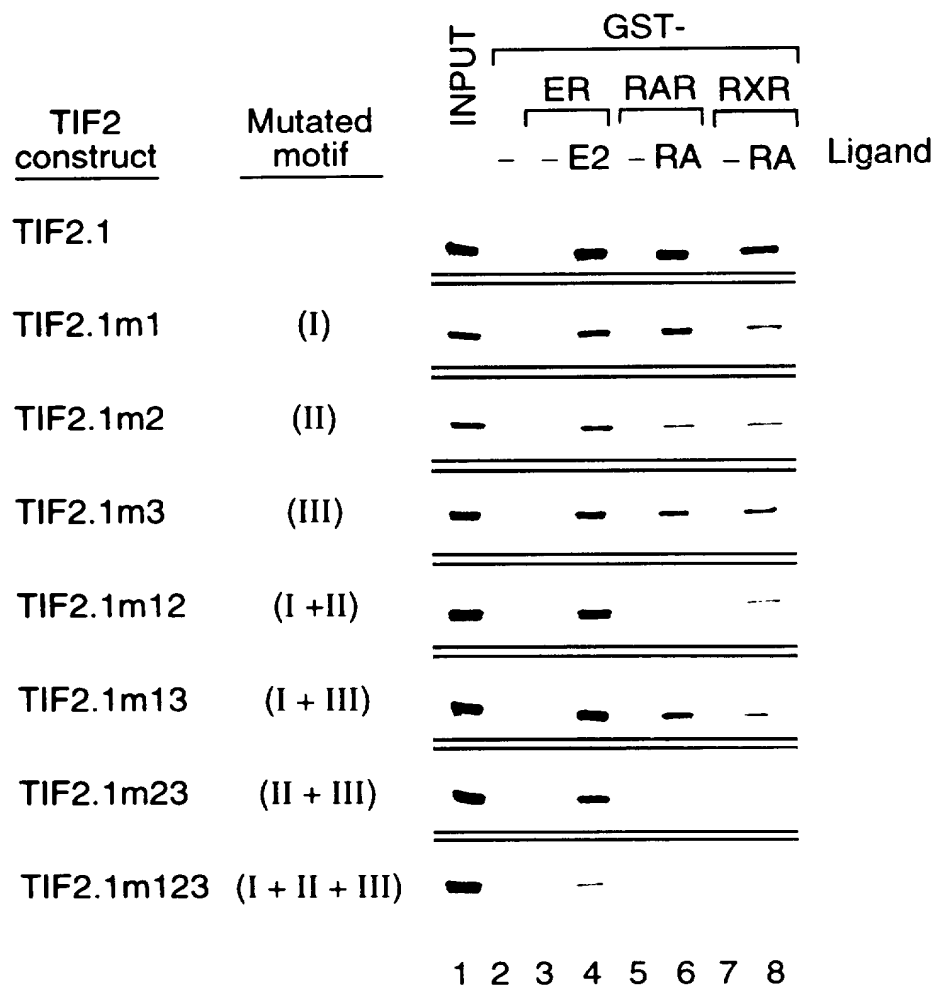


FIG.8D

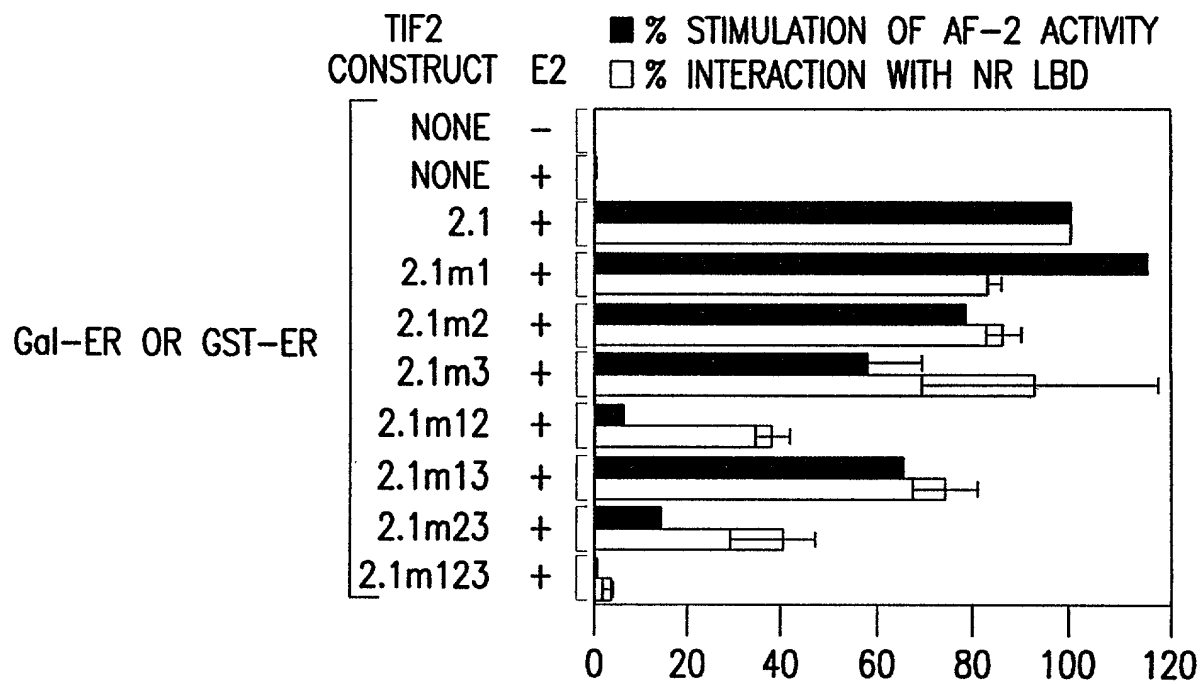


FIG.8E

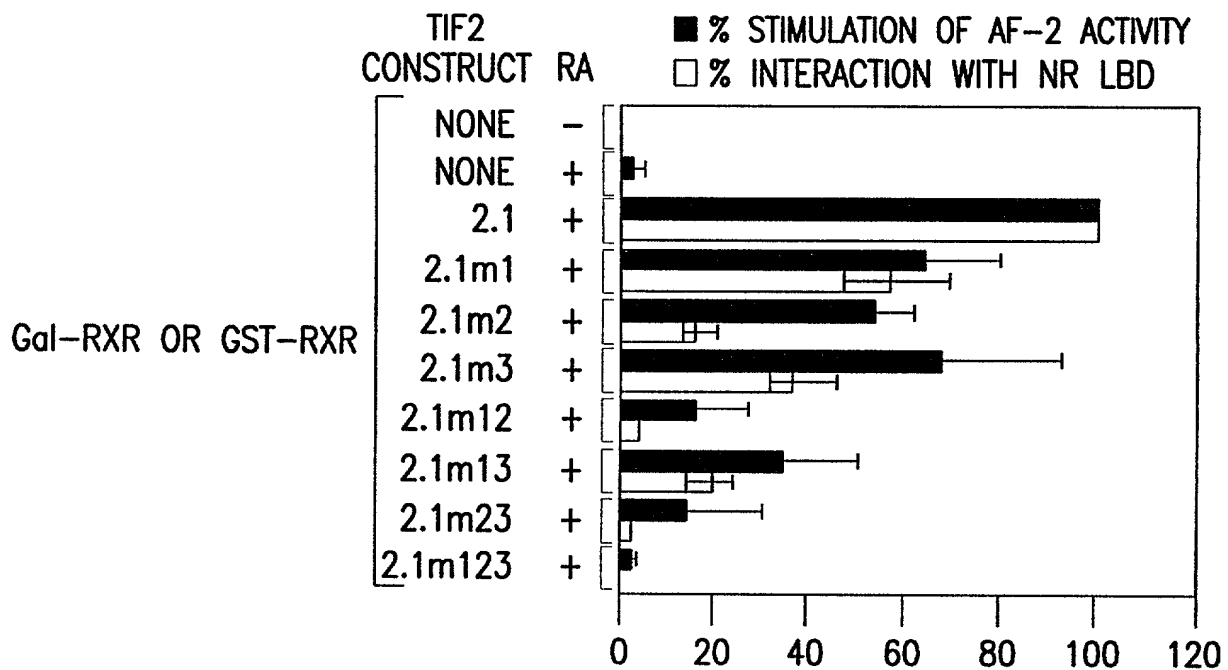


FIG.8F

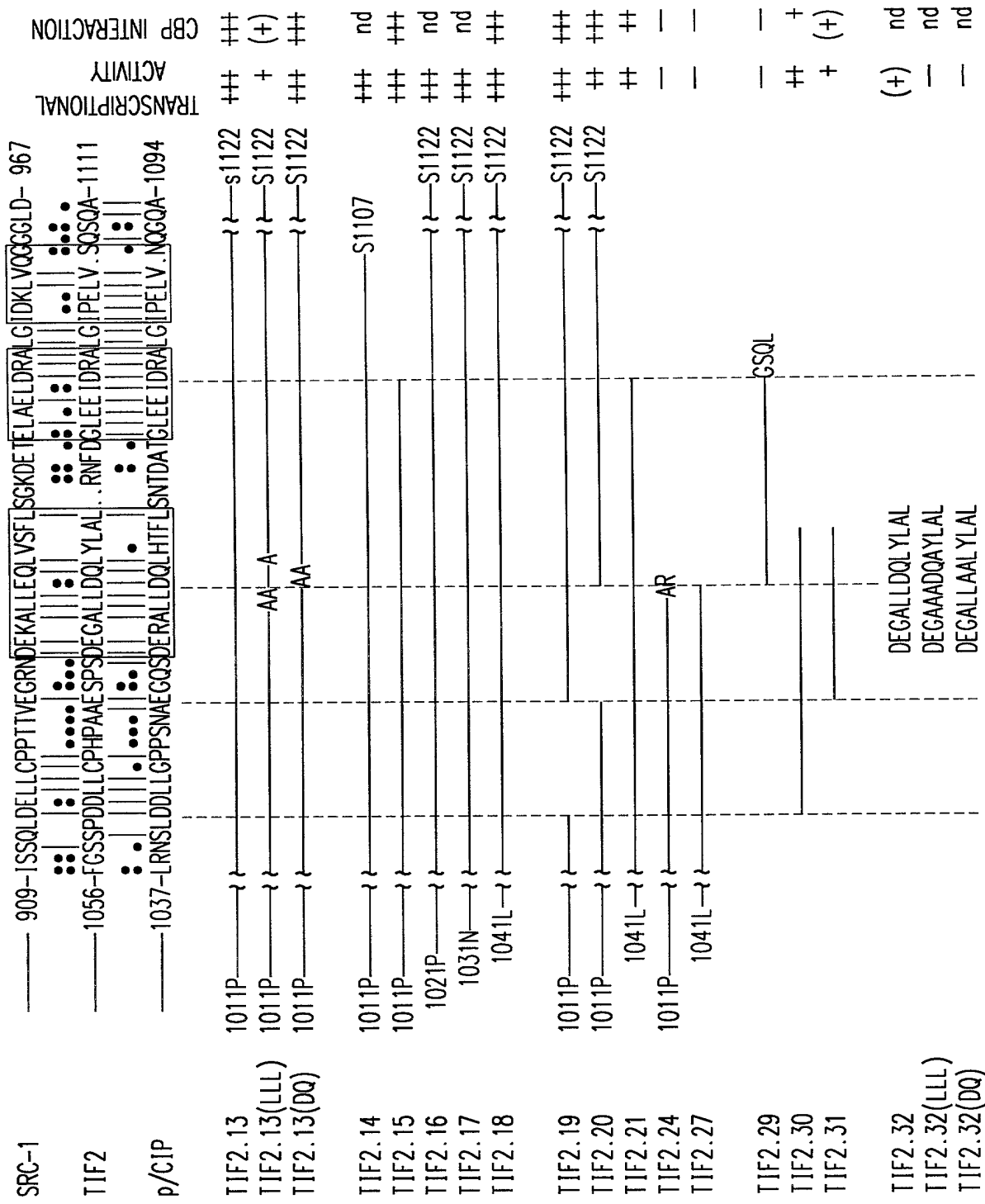


FIG.9A

Fold Induction of  
(17m)5-TATA-CAT

GAL-TIF	[			
	<u>Cos-1</u>		<u>HeLa</u>	
2.13	462	± 9	704	± 33
2.14	392	± 13	674	± 23
2.15	279	± 21	316	± 49
2.16	390	± 34	597	± 54
2.17	389	± 50	581	± 58
2.18	314	± 16	432	± 19
2.19	341	± 67	777	± 30
2.20	107	± 11	314	± 27
2.21	129	± 8	173	± 22
2.24	< 2		< 2	
2.27	< 2		< 2	
2.29	< 2		< 2	
2.30	98	± 13	117	± 6
2.31	35	± 3	34	± 3
2.32	2.8 ± 0.2		5.9 ± 0.9	
2.32(LLL)	1.4 ± 0.2		1.5 ± 0.1	
2.32(DQ)	1.7 ± 0.3		1.2 ± 0.2	

FIG.9B



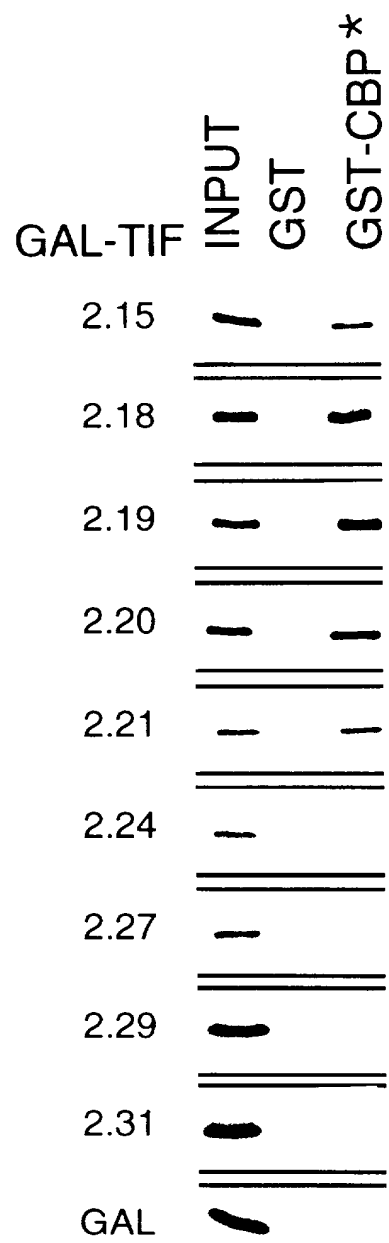
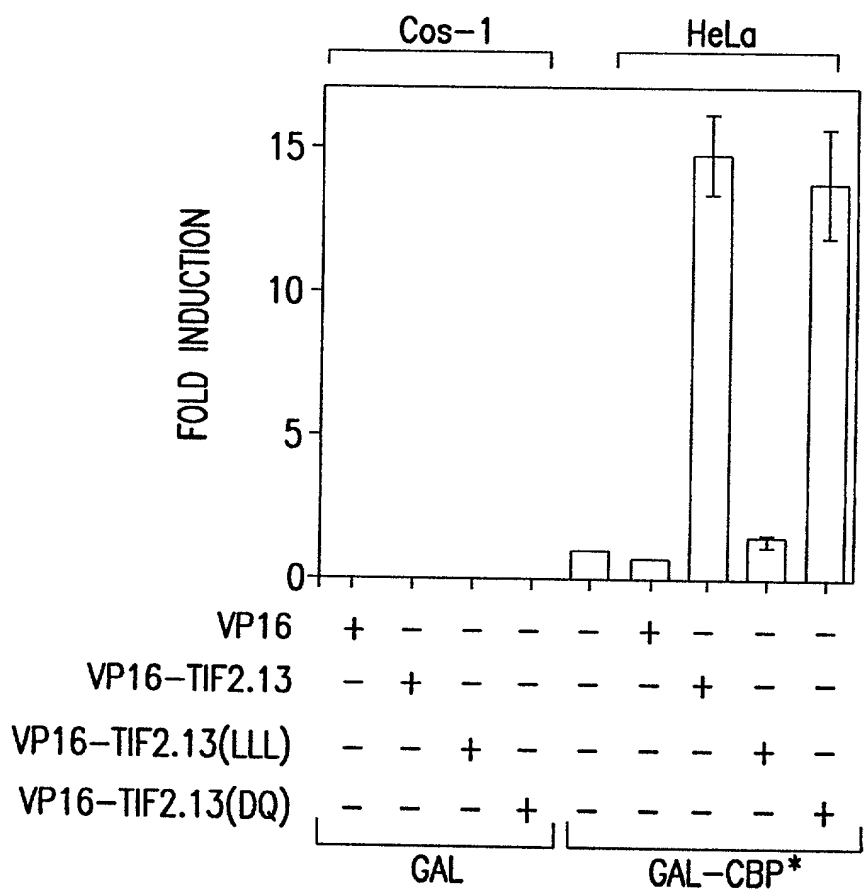
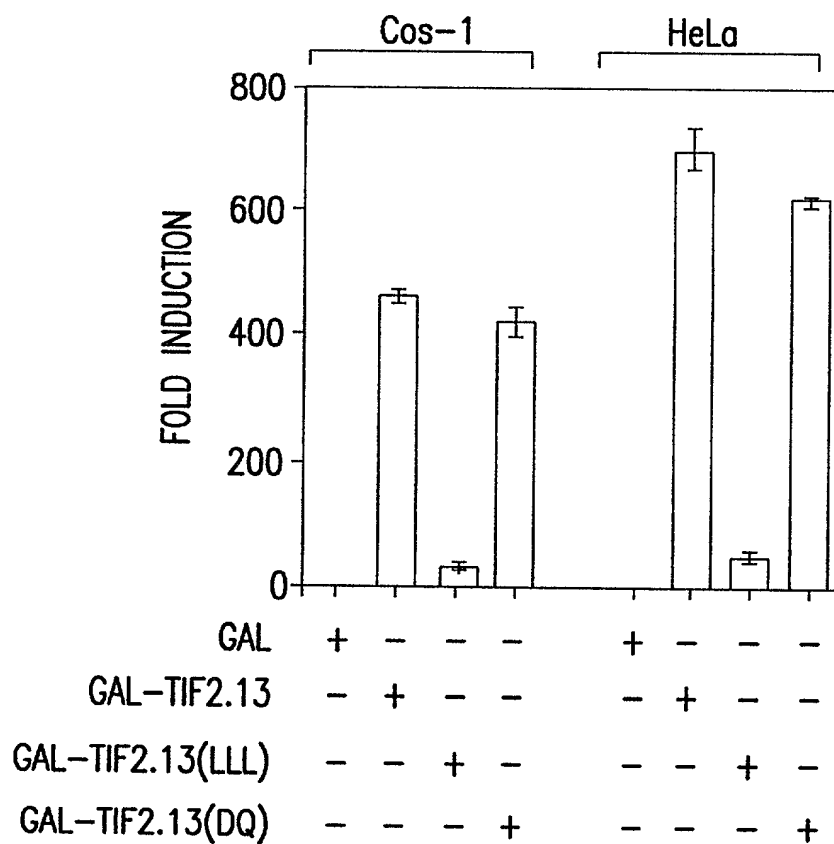


FIG.9C



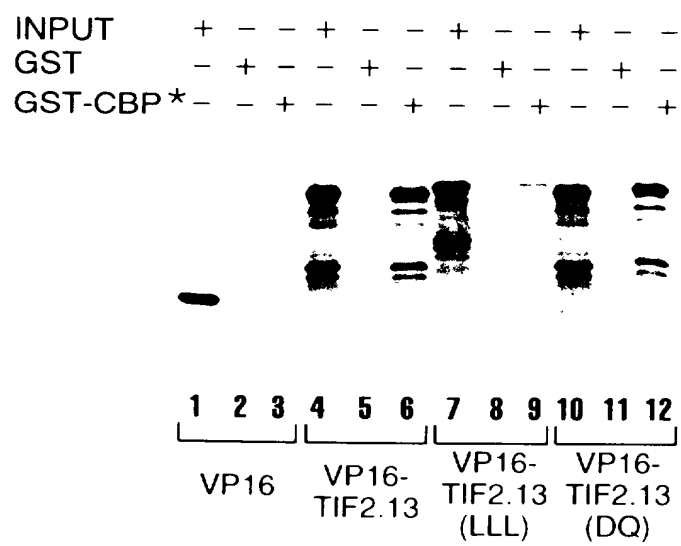


FIG.10C

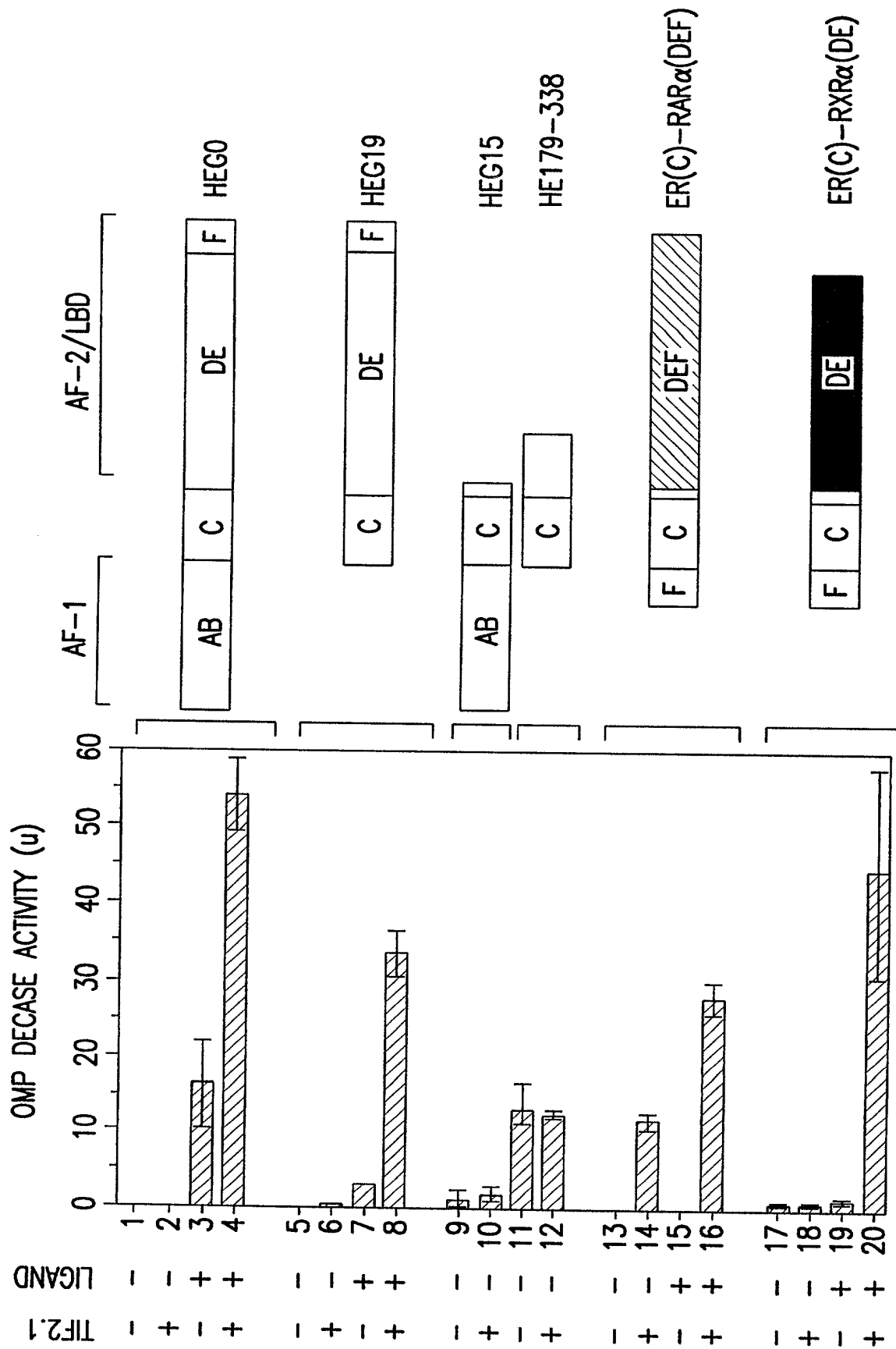


FIG.11

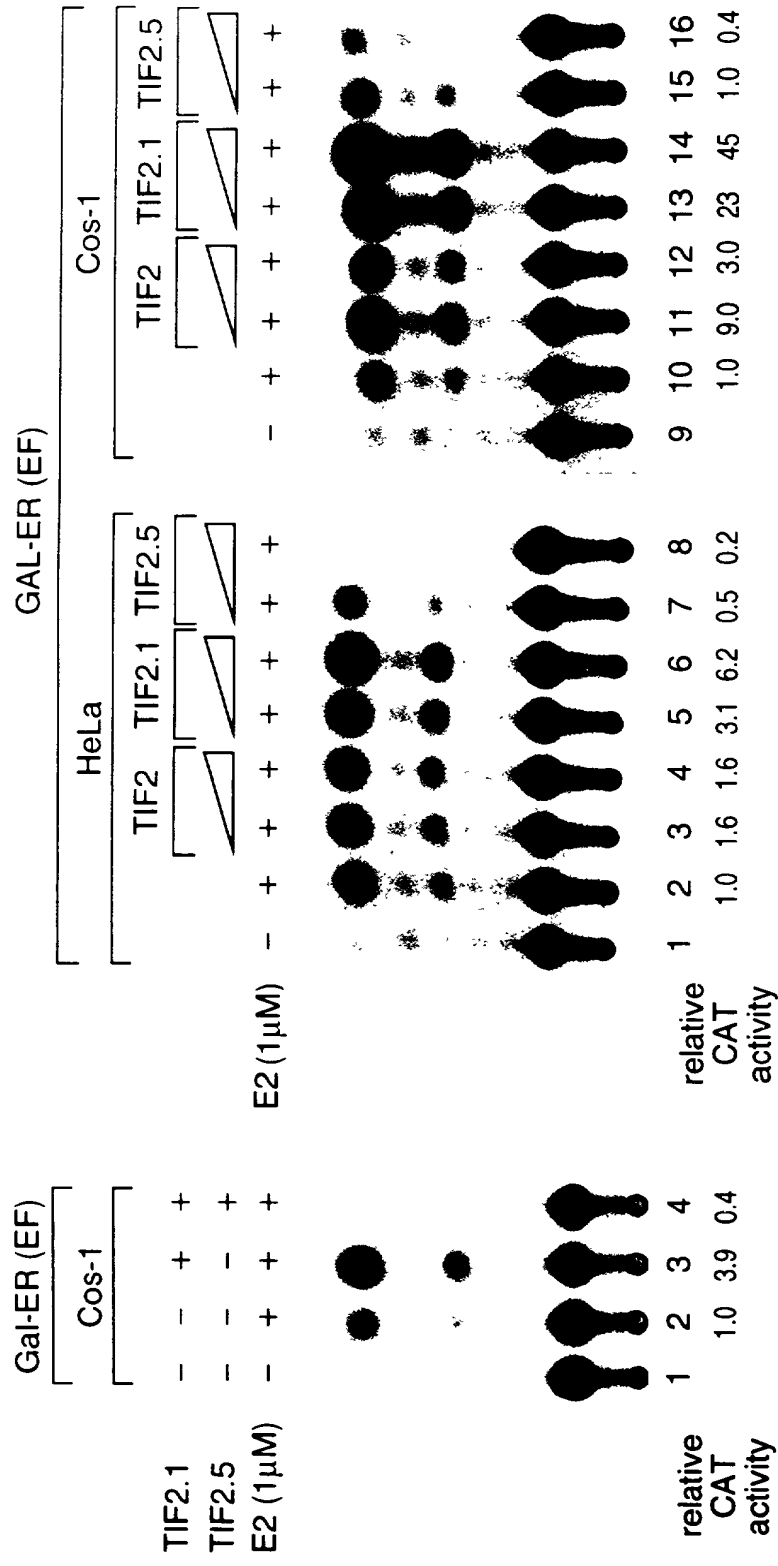


FIG.12B

FIG.12A

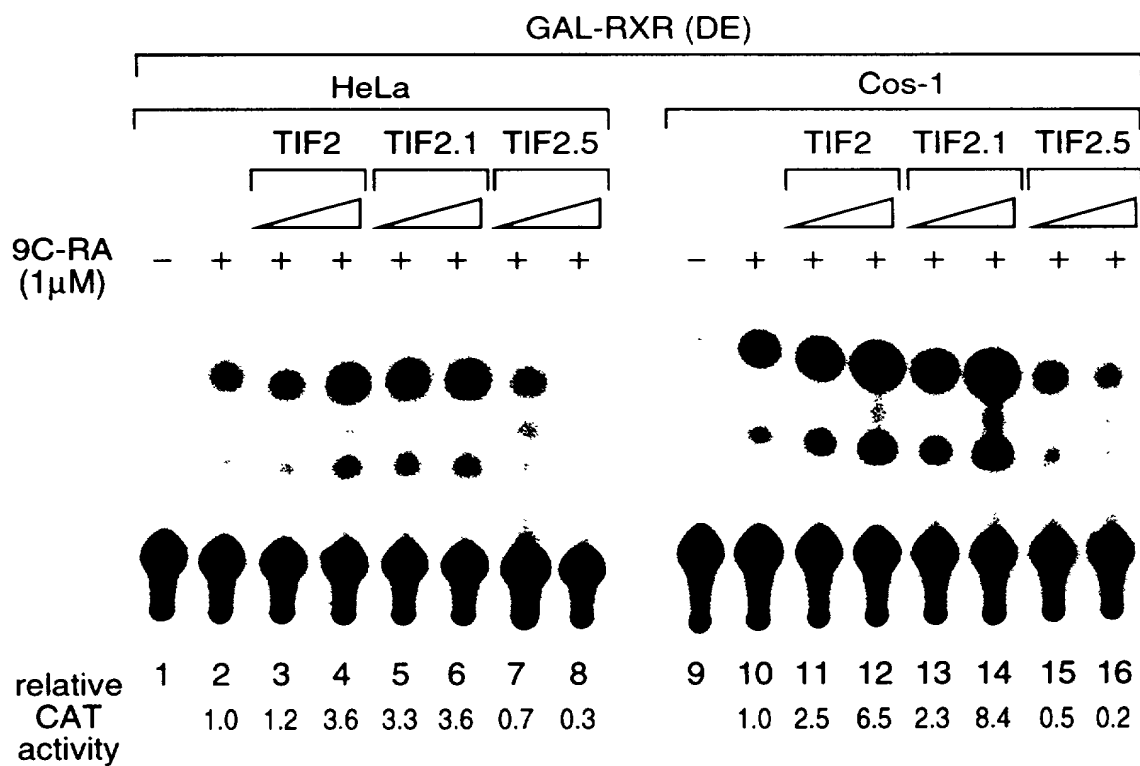


FIG.12C

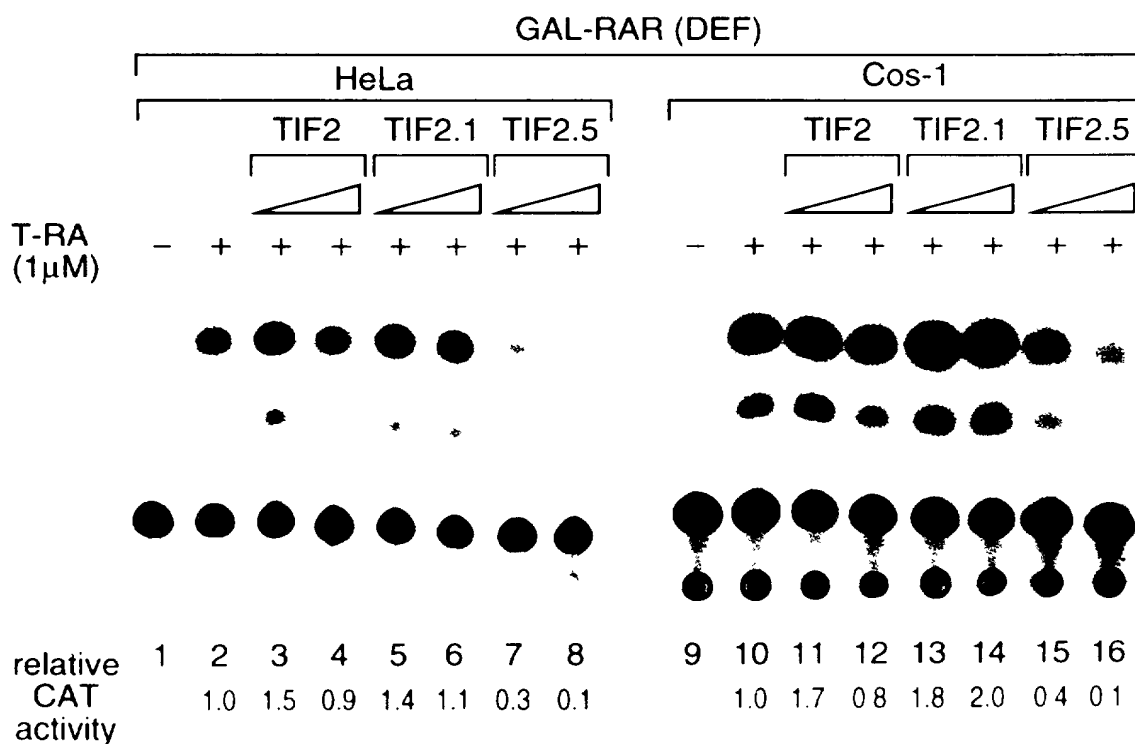


FIG.12D